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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 12:19:36 ; Search time 54.54 Seconds (without alignments) 7214.978 Million cell updates/sec

Title: Perfect score: US-09-722-377-2 1602

Scoring table: OLIGO\_NUC Gapop 60.0 , Gapext 60.0

atgtcggacaaaaaaggggt.....tttccttcagccagggatga 1602

Sequence:

Searched: 383533 seqs, 122816752 residues

Word size : 300

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*

1. /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
2. /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
3. /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
4. /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
5. /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
6. /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

No matches found

Search completed: July 23, 2002, 13:31:29 Job time: 4313 sec

```
Date: US-09-722-377-1 to: Issued_Patents_NA:* out_format : pfs

Date: Jul 23, 2002 3:37 PM

About: Results were produced by the GenCore software, version 4.5,

Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL-Frame+_P2n.model -DEV-xlh
-Q-/CGn2_JUSFTO_Spool/US09722377/runat_19072002_111535_29853/app_query.fasta_1.597
-DB-Issued_Patents_NA -OPMT-fastap -SUFFIX--01.ini -GAPOP-4.500
-GAPOP-4.500 -DEATT-0.050 -MARMARCH-0.100 -LOOPEXT-0.000
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-60.000 -VGAPEXT-60.000
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-60.000 -VGAPEXT-60.000
-FRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_MIN_900 -ALIGN-150 -MARINIX-011go
-TRR.MS-900 -MINLEN-0 -MAXLEN-200000000
-USCAP-1 - MARINIX-011go
-USCAP-1300 -MINLEN-0 -MAXLEN-200000000
-USCAP-1 - NORM-ext
-HEAPSIZE-500 -MAXLEN-200000000
-USCAP-1 - NORM-Ext
-HEAPSIZE-500 -MAXLEN-200000000
-MAXLEN-200000000
-MAXLEN-200000000
-MAXLEN-200000000
-MAXL
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RESULT
BE519781
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  ACCESSION
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                                                                                                                                                           570
570
479
451
BE519781 700 bp mRNA linear EST 23-OCT-2001 HV_CEB6021D05f Hordeum vulgare seedling green leaf EST library HV_CEB6021D05f, mRNA sequence.

BE519781
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11:
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                                                                                                                                                           35.6
29.9
28.2
22.2
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1602
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Copyright (c) 1993 - 2000 Comp
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em_estpl:*
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em_gss_vrt:*
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669
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AV835197 AV835197
AV945501 AV945501
BE558835 HV_CEb002
                                                                                                                                                           AV945620 AV945620
                                                                                                                                                                                                                                       Description
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Query Match

Matches 650;

Conservative

0;

Mismatches

Local Similarity

40.6%; 100.0%;

Score 650; Pred. No.

DB 10; 0; es 0;

Length 700; Indels

0,

Gaps

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VERSION
KEYWORDS
BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Aug 8, 2000 this sequence version replaced gi:9743969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wing.R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE519781.2 GI:13266203
EST.
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Total hq bases = 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: AATTAACCCTCACTAAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticeae;
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                                  149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence start: 4 quality sequence stop: 664.
                                                                                                                                                                                                                                                                                                                 C.I. 16151 (Mla6) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate 5874 (AvrMla6) of Blumeria graminis f. sp. hordel, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum Palmer, Frisch, Atkins and Wing). Plasmid DNA personned at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of
                       Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gapages/bgn/31/cover.html) 210 c 191 g 150 t
                                                                                                                                                      this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                                                                                                                                                                                                                                                          phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                           http://www.genome.clemson.edu/projects/barley. To order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="HY_CED0021D05f"
/clone_lib="Hordeum vulgare seedling green leaf EST
/clorey HycomA0005 (Blumeria challenged)"
/tissue_type="seedling green leaf"
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source

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RESULT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barley EST sequencing project in NIG and Okayama Unpublished (2001)
Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
                                                                                                                                                                                                                                                                                                                                                  AV835197 605 bp mRNA linear EST 22-JUN-2001 AV835197 K. Sato unpublished cDNA library: Hordeum vulgare subsp. spontaneum top three leaves adult, heading stage Hordeum vulgare subsp. spontaneum cDNA clone bah26o13, mRNA sequence.

AV835197
                                                                                                                                                                                                                                              Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                            Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato,K., Saisho,D., Takeda,K., Shini,T. an
                                                                                                                                                                                                                                                                                                                                     AV835197.1 GI:14527286
                                  submission;
          database:http://www.shigen.nig.ac.jp/barley/Barley.html
                                                                                                                                                                                                                                     Triticeae;
                                                                                                                                                                                                                 (bases 1 to 605)
Location/Qualifiers
                                                                                                                                                                                                                                     Hordeum.
                                                and Kohara, Y. Direct
                                                                                                                                                                                    Okayama Univ
                                                                                                                                                                                                                                                     Poaceae; Pooideae
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Best Local 9
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                                                                                                                                                                                            GCCTCCCGCTGTGGGGGTGTGGCGATCCTCA 605
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                                                                                                                                                                                                                                                                                                                                                570;
                                                                                     AV945501 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontan cDNA clone bah26013 3', mRNA sequence.
                                                           AV945501.1 GI:18241298
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                      EST
                                    Hordeum vulgare subsp.
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ilarity 100.0%;
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/db_xref="taxon:77009"
/clone="bah26013"
/clone_lib="K. Sato unpublished
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/dev_stage="adult, heading stage"
188 c 163 g 122 t
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/organism-"Hordeum vulgare subsp.
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Pred. No. 9.4e-276;
                                       spontaneum
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Triticeae;

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                               gcgctcaccaactggcggaacacggccaaggagaagaagaagtccgagacacggacatg 1314
                                                                                                                                                                                                                                        cggggctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccag 1434
                                                                                                                                                                                                                                                                                             ctgatggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagc 1374
                                                                                                                                                                                                                                                                                                                                    GCGCTCACCAACTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATG
                                                                                                                                                                                                                             CGGGGCTCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGACCCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                         BE558835 798 bp
HV_CEb0020108f Hordeum vulgare se
HVcDNA0005 (Blumeria challenged)
                V
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                CED0020108f,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="K. Sato unpublished cDNA library, adult, heading stage top three leaves" /tissue_type="top three leaves" /dev_stage="adult, heading stage" /dev_stage="adult, heading stage" 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="H602"
/db_xref="taxon:77009"
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99.8%;
                mRNA sequence
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Pred. No. 6.7e-230;
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                                                   798 bp
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                          p mRNA linear EST 23-OCT-2001
seedling green leaf EST library
d) Hordeum vulgare cDNA clone
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QV

1 atgtcggacaaaaaaggggtgccggcggggagctgccggagacgccgtcgtgggcggtg 60

Matches

Conservative

0;

Query Match
Best Local Similarity

28.2%;

Score 451; DB Pred. No. 8.9e 0; Mismatches

DB 10; B.9e-216; hes 1;

Length 798; Indels

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Clemson University
1100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total hq bases = 458
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 561.
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Fax: 864 656 4293
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                  /lab_nost="SULK"
/note="Note" SULK"
C.I. 16151 (Mla6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874 (AvrMla6
green seedlings were challenged with isolate 5874 (AvrMla6
) of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wei, Wise). In the TJ Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give pBluescript SK(-) cDNA
phagemids (Choi, Close). Phagemids were plated and picked
at the Clemson University Genomics Institute (CUGI) (Begum
, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/projects/barley. To
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
153 a 244 c 241 g 158 t
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/cultivar="CII6151 (Mla6)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Hordeum vulgare seedling green leaf EST
library HVcDNA0005 (Blumeria challenged)"
/tissue_type="seedling green leaf"
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AV945620/c
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                                                                                                                                                                                                                                            Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                 Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiklantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                      Contact: Tadasu Shin-i
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/organism-...-
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/clone_lib="K. Sato unpublished cDNA library, stadult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/dev_stage="adult, heading stage"
116 c 127 g 96 t 3 others
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Location/Qualifiers
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  61
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                                         ccgagccggggctcatcacccgtgcacctgcttcacaagggcatgggggggtcggacgac
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GTGGTGGCGCACCCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTC 6
                                                                                      CCGAGCCGGGGCTCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGAC
                                                                                                                                                                                                                                                              22.2%; Score 356; DB 9; Liarity 100.0%; Pred. No. 5.4e-168; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                      Length 402;
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Search completed: July 23, Job time: 5009 sec 2002, 12:50:50

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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  heat shock protein nuclear factor I - hypothetical prote conserved hypothet
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C; Species: Hordeum vulgare (barley)
C; Species: Hordeum vulgare (barley)
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change |
C; Accession: 704481
R; Panstruga, R.; Buschges, R.; Piffanelli, P.; Schulze-lefet, P.
Nucleic Acids Res. 26, 1056-1065, 1998
A; Title: A contiguous 60bb genomic stretch from barley reveals mc A; Reference number: 215372; MUID:98128007
A; Recession: 704481
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T04481
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                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-533 <PAN>
A;Cross-references: EMBL:Y14573; NID:g2894376; PIDN:CAA74909.1; PID:g2894377
                                                                                                                                                                                                                                                                                                                                                                A; Gene: Mlo
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## ALIGNMENTS

from barley reveals molecular evidence

for

15-Jun-2001

	A;Map position: 4 A;Map position: 4 A;Introns: 43/3; 116/3; 155/3; 176/1; 204/3; 229/3; 259/2; 276/1; 289/3; 359/3; 402/3 C;Superfamily: barley pathogen resistance protein Mlo
	Ouery Match 100.0%; Score 2788; DB 2; Length 533; Best Local Similarity 100.0%; Pred. No. 5.9e-232; Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
·	Qy 1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60 
	Qy 61 KAELMLVGFTSLLLIVTQDPIIAKICISEDAADVMMPCKRGTEGRKPSKYVDYCPEGKVA 120
	OT VEHILLE OF TOWNS AND A SECOND OF THE SECO
	Qy 121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
	Db 121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKNRTWKKWETETTSLEYQFANDPARF 180
	Qy 181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
	Db 181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
	Qy 241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
	Db 241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
	Qy 301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQNAHFVWTVA 360
	Db 301 IIMEMALEIQDRASVIKGAPVVEPSNKEFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360
	Qy 361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420

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A;Cross references: EMBL:295496; PIDN:CAB08860.
A;Experimental source: cv. Igri
C;Genetics:
A;Gene: Mlo-hl
A;Map position: 4H
A;Map position: 4H
A;Introns: 41/3; 139/3; 178/3; 199/1; 282/2; 29
C;Superfamily: barley pathogen resistance prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001 C;Accession: T05952
R;Panstruga, R.
submitted to the EMBL Data Library, May 1997
A;Reference number: Z15093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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A;Accession: T05952
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-544 <PAND

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T05952
Mlo-hl protein -
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                                               464 VHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADI 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------VDYC-PEGKVALMSTGSLHQLHVF1FVLAVFHVTYSVITIALSRLKMRTWKKWE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISLLLIVTQDP-VSRICISKEAGEKMLPCKPYDGAGGGKGKDNHRRLLWLQGESETHRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWI
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                                                                                                                                  GSNMKRSIFDEOTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSP 463
                                                                                                                                                                                                                                        TLEQNAFOMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQELCSYMTFPLYALVTQM 403
                                                                                                                                                                                                                                                                                                                                                                                                                         GSHMKRSIFDEQTAKALTNWRKMAKEKKKARDAAMLMAQMGGGAT-----PSVGSSP
                                                                                                                                                                                                               TLFQNAFQMAHFVWTVATPGLKKCYHEKMAMSIAKVVLGVAAQILCSYITFPLYALVTQM
  VHLLHKAGARSDDPQSVPASPRAEKEGGG----
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Pred. No. 5.3e
51; Mismatches
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     -VQHPARKVPPCDGWRSASSPALDAHI
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probable mlo protein - rice (;Species: Oryza sativa (rice) (;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001 C;Accession: T03797 R;Panstruga, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: Z15093
A; Accession: T03797
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C; Superfamily: barley pathogen resistance protein Mio
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A; Residues: 1-537 < PAN>
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                                                                                                                                                                                                                                                                                                                                                                                   SRELPETPTWAVAVVCAVLVLVSAAMEHGLHNLSH-----KTTAEVLIFLVLSALAEL
                                                                                                                          DFSFS 531
                                       IFEEQTMKALMNWRKKAMEKKKVRDADAFLAQMSVDF----ATPASSRSASPVHLLQDH
                                                                                           IFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKG
DFSFS
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ce: isolate IR-BB21
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Pred. No. 3.5e-146;
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RESULT

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hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C;Accession: B86247
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719
A;Accession: B86247
A;Accession: B86247
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A;Map position: 1
C;Superfamily: barley pathogen resistance protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVITIALSRLKMRTWKKWETETTSLEYQEANDPARFRETHQTSFVKRHLGL-SSTPGIRW
                                   VHRL-NPNDRRRSASSS-----ALEADIP-----
                                                                                                                                                       GAVVQILCSYVTLPLYALVTQMGSKMKPTVFNDRVATALKKWHHTAKNETK------HG
                                                                                                                                                                                                                              VQPGDDLFWFGKPRFILFLIHLVLFTNAFQLAFFAWSTYEFNLNNCFHESTADVVIRLVV
                                                                                                                                                                                                                                                      VEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIVTYAFGKIKMRTWKSWEEETKTIEYQYSNDPERFRFARDTSFGRRHLNFWSKTRVTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EHQFWDPESQHQEAETSTHHSLAHESSEPVLASVELPPIRTSKSLRDFSFKK 573
                                                                         RHSGSNTPFSSRPTTPTHGSSPIHLLHNFNNRS--VENYPSSPSPRYSGH-----
                                                                                                             QMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHP 501
                                                                                                                                                                                         GLALQFICSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMA 441
                                                                                                                                                                                                                                                                                                        IMFVAVLELLINSYGLRSYLWLPFIPLVVILIVGTKLEVIITKLGLRIQEKGDVVRGAPV
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                                       -----SADFSFSQ 532
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war, K.;
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RESULT H96640

> RESULT T02582

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hypothetical protein T25B24.9 [imported] - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001 C;Accession: H96640 (C;Chaccession: Hecker, J.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Duansen, N.F.; Hughes, B.; Huizar, L. (Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Duansen, N.F.; Hughes, B.; Huizar, L. (Chin, C.W.; Huizar, L.) (Chin, C.W.; Huizar, L.) (Chin, C.W.; Huizar, L.) (Chin, C.W.; Huizar, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. (C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; I Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. (Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. (Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. (Rizzo, M.; Ru, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis. A; Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
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A; Residues: 1-583 <STO>
A; Cross-references: GB:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A86141; MUID:21016719
A;Accession: H96640
A;Status: preliminary
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C; Superfamily: barley
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                      VAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYALGKTKMRRWKKWEEETKTIEYQYSHDPERFRFARDTSFGRRHLSFWSKSTITLWIVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIR-WVVA 206
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                                                                                                                          GDATPSRGSSPMPSRGSSPVHLL----HKGMGRSDDPQSAPTSPR-----TQQEA 490
                                                                                                                                                                     VQILCSYVTLPLYALVTQMGSKMKPTVFNERVATALKSWHHTAKKNIKHGRTS-----
                                                                                                                                                                                                                                                         GDHFFWFGRPRFILFLIHLVLFTNAFQLAFFVWSTYEFGLKNCFHESRVDVIIRISIGLL
                                                                                                                                                                                                                                                                                                                                                  IAVLFLLTNTNGLNSYLWLPF1PF1VILIVGTKLQVIITKLGLRIQEKGDVVKGTPLVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                 FFRQFFRSVTKVDYLTLRHGFIMAHLAPGSDARFDFRKYIQRSLEEDFKTIVEINPVIWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFRQFFRSVTKVDYLTLRAGFINAHLSQNS--KFDFHKYIKRSMEDDFKVVVGISLPLWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAELMLMGFISLLLTIGQG-YISNICIPKNIAASMHPCSASEEARKYGKKDVPKEDEEEN 117
                                        RDMYPVVVAHPVH---RLNPNDRRRSASSSALE---
                                                                                   ESTTPFSSRPTTPTHGSSPIHLLRNAPHKRSRSVDESFANSFSPRNSDFDSWDPESQHET
                                                                                                                                                                                                              LQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMI 444
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-TSNSNHRSRFGEEESEKKFVSSSVELPPGPGQIRTQHEISTISLRDFSFKR 583
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Pred. No. 4e-98;
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H. vulgare Mlo protein homolog [imported] - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 15-Jun-2001 C;Accession: T02582; D84814 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, August 1998 A;Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence. A;Reference number: Z14679 A;Reference number: Z14679 A;Ressidues: Tanslated from GB/EMBL/DDBJ A;Residues: 1-570 <ROUNA;Ressidues: 1-570 <ROUNA;Ressidues:
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-570 <STO>
A;Cross references: GB:AE002093; NID:g3402694; PIDN:AAC28997.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g39200; T16B24.16
A;Molecule type: DNA
A;Genetics:
A;Genetics: 34,320,000
A;Molecule type: DNA
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A;Experimental source: cultivar Columbia
                                                                                                      468
                                                                                                                                                                                     455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 VGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTE------GRK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 VPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELML 66
                                                                                                 TTPTHGMSPVHLLHNYNNRSLDQQTSFTASPSPPRFSDYSGQGH----GHQ-HFFDPESQ 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVVAFFRQFFRSVT 216
                                                                                                                                                                                PMPSRGSSPVHLLHKGMGRSDDPQ----SAPTSPRTQQEARDMYPVVVAHPVHRLNPNDR 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYSPRRNLATKGYDKCAEKGKVALVSAYGIHQLHIFIFVLAVFHVLYCIITYALGKTKMK 181
                                                                                                                                                                                                                                                                                                                                                            PLYALVTOMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSS 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFILFLIHLVLFTNAFQLAFFVWSTYEFTLKNCFHHKTEDIAIRITMGVLIQVLCSYITL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYNTF 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVDYLTLRHGFIMAHLPAGSAAREDFQKYIERSLEQDFTVVVGISPLIWCIAVLFILTNT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVDYLTLRAGFINAHLSQNS--KFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PSKYVDYCPE-GKVALMSTGSLHQLHVF1FVLAVFHVTYSV1T1ALSRLKMR 157
                                                                                                                                                                                                                                                                        PLYALVTQMGTSMRPTIFNDRVANALKKWHHTAKKQTKHGHS------GSNTPHSSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGWDSYLWLPFLPLIVILIVGAKLQMIISKLGLRIQEKGDVVKGAPVVEPGDDLFWFGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWKSWERETKTIEYQYANDPERFRFARDTSFGRRHLNIWSKSTFTLWI-----FFGSVT
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similar to Mlo proteins from H. vulgare [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
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A;Gene: At2g33670
A;Map position: 2
C;Superfamily: barley pathogen resistance protein Mlo
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
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A;Molecule type: DNA
A;Residues: 1-501 <STO>
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A; Accession: B84748
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                                                                                                                                                                                                                                                                                                                                                                                                                         285 FIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLT
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                                                                                                                STMKRSVFDDQTSKALKNWHKNAKKKSE--
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GDIESASPANI -----TASVDVKESDQSQSRDL
                                                          --- RGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDM
                                                                                                                                                                           SNMKRSIFDEQTSKALTNWRNTAKEKKKYRDTDMLMAQMIGDATPSRGSSPMPS-----
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C;Accession: F84552
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A.; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: F84552
A;Accession: F8457
A;Accession: F8457
A;Accession: F84580
A;Residues: 1-574 <STO>
A;Cross-references: GB:AE002093; NID:g4914369; PIDN:AAD32905.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2917480
A;Map position: 2
C;Superfamily: barley pathogen resistance protein Mlo
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Similar to Mlo proteins from H. vulgare [imported] - Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001 C;Accession: B84552 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; KOO, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Mierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
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                                                                                                                                                                                                                                              VVVAHPVHRLNPNDRRRSASSSALEADIPSADFSF 530
                                                                                                                                                                                                                                                                                                                                                       LYALVTQMGSRMKKSVFDEQTSKALKKWRMAVKKKKGVKATTKRLG---GDGSASPTAST 484
                                                                                                                                                                                                                                                                                                                                                                       LYALVTOMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSP 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVLEFIHLTLEQNAEQMAHEVWTVATPGLKKCYHTQIGLSIMKVVVGLALQELCSYMTEP 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRTDYLTLRNGFIAVHLAPGSQFNFQKYIKRSLEDDFKVVVGVSPVLWGSFVLFLLLNID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDIN 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGWKHWENETSSHNYEFSTDTSRFRLTHETSFVRAHTSFWTRIPFFFYVGCFFRQFFRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVVAFFRQFFRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELMLVGFISLLIVTQDPIIAKICISEDAADVMWPC-----KRGTEGRK-----
                                                                                                                                                                                                                                                                                  VRSTSSVRSLQRYKTTPHSMRYEGL----DPETSDLDTDNEALTPPKSPPS---
                                                                                                                                                                                                                                                                                                                   MPSRGS------SPVHLLHKGMGRSDDPQSA-----PTSPRTQQEARDMYP 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                             -KVEPNKTNTGETSRDTETD--SKEFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.0%; Score 1088; 42.6%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86;
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1.6e-85;
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                                      C.Y.;
lon, L.
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: B84552
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-580 <STO>
A;Cross-references: GB:AE002093; NID:g6598336; PIDN:AAB86520.2; GSPDB:GN00139
C;Genetics:
A;Gene: At2g17430
A;Map position: 2
C;Superfamily: barley pathogen resistance protein Mlo
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.B. ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, Rizzo, M.; Rooney, T.; Liu, S.X.; Liu, S.A.; Lucos, J.S.; Maiti, F. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Accession: E96495

A; Status: preliminary
                                                                                                                                                                                                                                                   hypothetical protein F8D11.2 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 **sequence_revision 02-Mar-2001 **text_change 15 C;Accession: E96495 C;Accession: E96495 A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, Cchin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cr
                                                                                                                                                                                                                                                                                                                                                                                        RESULT
E96495
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------WFQHRHKKALWEALEKMKAELMLVGFISLLLIVTQDPIIAKICISEDAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAPSGGKELSQTPTWAVAVVCTFLILISHLLEKGLQRLANVCFLLLLLLFLRVFLFKHSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPYLWASFVIFLLENVNGWRTLFWASIPPLLIILAVGTKLQAIMATMALEIVETHAVVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMWPC-KRGT---EGRKPSKYVDY------CPEGKVALMSTGSLHQLHVFIFVLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFFFYVGCFFRQFFVSVERTDYLTLRHGFISAHLAPGRKFNFQRYIKRSLEDDFKLVVGI
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45.7%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                             15-Jun-2001
                                                                                                                                                                                                                                                                               S.; White,
                                                                                                                                                                   Khaykin, E.;
Maiti, R.; M
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                                                                                                                           Η.;
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                                                                                                                                                                                                                                                              Dewar,
                                                                                                                                                                     .; Kim,
Marzia
                                                                                                                           Tallo
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A;Reference number: Z14248
A;Accession: T01089
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-526 <KAP>
A;Cross-references: EMBL:AC002330; NID:g2262135; PID:g3892049
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T10P11.12 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 15-Jun-2001 C;Accession: T01089
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C:Superfamily: barley pathogen resistance protein
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                                                                                                                 A; Introns: 61/1;
A; Note: T10P11.12
                                                                                                                                                                                                                                                                                                                        R; Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Till, hi, M.; Martienssen, R.; Chen, E.Y.; Wilson, R.; McCombie, W.R. submitted to the EMBL Data Library, November 1998
A; Description: Sequence of A. thaliana BAC T10P11 from chromosome I
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                                                                                                                                                      A; Map position: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:AE005173; NID:g10092398; PIDN:AAG12804.1; GSPDB:GN00141;
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Best Local
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                    Query Match
Best Local
                                                                                              Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 TMKRSVFDEQTSKALEQWHKKARKKNE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IH-EQEMMNDPSRFRLTHETSFVREHVNSWASNKFFFYVMCFFRQILRSVRKSDYLTMRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFISVHLAPGMKFDFQKYIKRSLEDDFKVVVGIRPELWAFVMLFLLFDVHGWYVTAVITM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSLEYQFANDPARFRFTHQTSFVKRHL-GLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVGFISLLLIVTQDPIIAKICISEDAADVMWPC----KRGTEGRKPSKYVDY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEGPRQLDQTPTWAVSTVCGVIILISIILELIIHKVGEVFERKKKKALFEALEKIKNELM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGS 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPPLLTLAIGTKLQAIISYMALEIQERHAVIQGMPVVNVSDQHFWFEKPDLVLHMIHFVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- CPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETET 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLGFISLLLTFGQN-YIASICVPSRYGHAMSFCGPYDGPSEDDRKKLKKTDHAMRILYSV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218;
                                                                                            barley pathogen resistance protein
                                                                                                                                 145/3; 184/3; 205/1; 237/3; 262/3; 309/1; 322/3; 392/3; 415/2; 435/3
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                  33.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GLRSCFHHHFGLIIIRVCLGVGVQFLCSYITLPLYALVTQMGS
  79;
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                    Score 932.5;
Pred. No. 3.5
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Pred. No. 2.
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                                       DB 2;
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H. vulgare Mlo protein homolog At2g44110 (imported] - Arabidopsis thallana R;Alternate names: hypothetical protein f6E13.24 C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 15-Jun-2001 C;Accession: T00691; E84874 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R;submitted to the EMBL Data Library, June 1998 A;Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
                                                                                                                                                                                                                                                                                            A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, X.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Map position: 2
A;Introns: 39/3; 59/1; 132/3; 1
C;Superfamily: barley pathogen
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                                                                           A; Gene: F6E13.24; At2g44110
                                                                                                A;Cross-references: GB:AE002093; NID:g3212880; PIDN:AAC23431.1; C;Genetics:
                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-496 <STO>
                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                        A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487 A;Accession: E84874
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: AC004005; NID: g3212846; PID: g3212880
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-496 < ROU>
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A; Accession: T00691
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       59/1; 132/3; 171/3; 193/3; 222/3; arley pathogen resistance protein N
       3; 247/3;
1 Mlo
                            277/2;
                                                                                                                                GSPDB:GN00139
                            294/1; 307/3; 377/3
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A;Residues: 1-429 <BEV>
A;Residues: 1-429 <BEV>
A;Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6.80
A;Experimental source: cultivar Columbia; BAC clone T22A6
C;Genetics:
A;Gene: ATSP:T22A6.80
A;Map position: 4
A;Introns: 40/3; 60/1; 87/3; 126/3; 151/3; 177/3; 202/3; 232/2;
C;Superfamily: barley pathogen resistance protein Mlo
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T09888
T09888
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Jun-2001
C;Accession: T09888
C;Accession: T09888
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mew
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                                                                  LHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAH 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKGAIFNEQTQEHLVGWAKMAKRGVKKGATQVGTSH---DATSPRPSIQLNS-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHL 466
                                LLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVALMSTGSLHQLH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205;
 LMLTVSQ-AAIRHICV--
                                                                                                                                              181;
                                                                                                                                                             Similarity
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                                                                                                                                            Conservative
                                                                                                                                                             30.6%; Score 853.5; DB 2; Length 429; 41.8%; Pred. No. 1.7e-65;
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                                                                                                                                              70;
                                                                                                                                              Mismatches 149;
   -PPAL-----GQVPLVSVEALHQLH
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                        232/2; 262/3; 331/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F18N11.50 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 15-Jun-2001 C;Accession: T47469
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                                                                                                                                                                                                                                                                                                                                                                                                      y Match 28.4%; Score 790.5; DB 2; Local Similarity 37.3%; Pred. No. 5.4e-60; hes 177; Conservative 90; Mismatches 158;
                                                                                                                                                                                                                                                              77
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                                                                                                                                                                                                                                                                                                                                  17 RSLQETPTWALATVCFFFIAVSICLERLINLLSTRLKKNRKTSLLEAVEKLKSVLMVLGF 76
                                                                                                                                                                                                                                                                                                                                                             10 RELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEKRSRAEEA-VITPSDELFWFHRPGIVLQLIHFILFQNSFEIAFFEWILFTYGIHSCIM 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYH
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                                                                                                                                                                                                                                                                                              ISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRK------PSKYVDYC- 114
                                                                                                                                    NSKEDEHKXIKRSMEDDEKVVVGISLPLWGVAILTLELDINGVGTLIWISEIPLVILLCV 294
                                                                                                                                                                                        SKGKTSLISEEGLTQLSYFFFVLACMHILCNLAILLLGMAKFFVYVIHIDE--KMEFVGE
         GTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAH
                                           NNAFNFQNYIQRSLHEDFKTVVGISPLMWLTVVIFMLLDVSGWRVYFYMSFVPLIIVLVI
                                                                                                                   -----NSGVSSSK-----RQFYNSVAKVDYLTLRHGFIFAHVSS
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**X** 

Mewes, H.W.;

Lemcke,

401

425

369

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162

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49;

Gaps

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354 290

Ωγ	탕	Qy	Db Qy	ОУ	ДЬ	B 8	Qy Db	D Q	Query Ma Best Loo Matches	A; Gen A; Map C; Sup	A; Sta A; Mol A; Res A; Cro	A; Auti ker, l A; Tit A; Ref	Natur A; Auti C.A.;	R;The Chin	RESULT H86393 protein C; Spec C; Date	Db .	Оу	Дb
377 MKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALINWRNTAKEKKK 432		317 KGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHEVWTVATPGLKKCYHTQIGLSI 376	260 LPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVI 316 270WLVLLVGAKLQHVIATLALENASITEYASGI 300	223 LRAGETNAHLSQNSKFDFHKYIKRSMEDDFKVVVGIS 259	163 ETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLT 222 	112DYCDEGKVALMSTGSLHOLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKW 162 	70 ISLLLIVTQDPIIAKICISED-AADVMMPC	10 RELPETPSWAVAVYFAAMVLVSVLMEHGLHKLGHWFQHRHKKALMEALEKMKAELMLVGF 69       : :         :::  : :  :   :   :	y Match 22.6%; Score 631; DB 2; Length 507; Local Similarity 33.0%; Pred. No. 3.1e-46; hes 157; Conservative 63; Mismatches 130; Indels 126; Gaps 12;	rfamily: barley pathogen resistance protein Mlo	us: prelininary cule type: DNA dues: 1-507 <570> s-references: GB:AE005172; NID:g9295722; PIDN:AAF87028.1; GSPDB:GN00141	A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  A; Reference number: A86141; MUID:21016719  A; Accession: H86393	408, 816-820, 2000 Ors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali M.; Rooney, T.; Rowley, D.; Sakano, H	Ligdis, A., Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. N.F.; Hughes, B.; Huizar, L.	RESULT 15 186393 186393 1970tein T24P13.8 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Dete: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001 C:Dete: 02-Mar-2001	412 FDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMDSRGSS 462	355 FVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSI 411 	: :  :    :  :  :     ::       ::  :

Db 357 LRLILGESGQELCSYSTLPLYALVTQMGTNYKAALLPQRVRETINGWGKATRRKRR 412

Search completed: July 23, 2002, 14:31:25 Job time: 480 sec

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Sequence
gb_pat:A92828
gb_pat:A92833
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Query: US-09-722-377-1
Query length: 533
Database: GenEmbl:*
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SOURCE
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AUTHORS
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-Q-/cgn2_1/USPTO_spool/US09722377/runat_19072002_111535_29796/app_query.fasta_1.597
-Q-(cgn2_1/USPTO_spool/US09723377/runat_19072002_111535_29796/app_query.fasta_1.500
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-PGAPEXT=7.000 -VGAPEXT=60.000
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Sequence 2 from Patent WO9804586.
A92828
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 1602)
Panstruga, R. and Bueschges, R.
POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
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! A92833 Sequence 7 from Patent
! Z83834 H.vulgare mRNA for Mic
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Align seg 1/1 to: A92828 from: 1 to: 1602
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                                      IleArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrLy
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Sequence 7 from Patent WO9804586.
A92833
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
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                                               775 ACCAGACGTCGTTCGTGAAGCGCCACCTGGGCCTCTCCAGCACCCCTGGC
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  201 IleArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrLy 217
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                                                                                                                                                                                                                          CTAAGCCGTCTCAAAATGAGAACATGGAAGAAATGGGAGACAGAGACCAC
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ProValHisArgLeuAsnProAsnAspArgArgArgSerAlaSerSerSe
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                                                                         roArgThrGlnGlnAlaArgAspMetTyrProValValValAlaHis
                                                                                                                                                                CGAGGCTCGTCGCCGATGCCGAGCCGGGGCTCATCACCCGTGCACCTGCT
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Frijters,A., van Daelen,R., van de Lee,T., Diergaarde,P.,
Groenendijk,J., Toepsch,S., Vos,P., Salamini,F. and
Schulze-Lefert,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (09-JAN-1997) Panstruga
Laboratory, Colney Lane, Norwich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The barley Mlo gene: a novel control element of plant pathogen resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.

1 (bases 1 to 1917)
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576
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EGRKPSKYVDYCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWK
KWETEFTSLEX/QFANDPAFFRETHQTSFVKRHLGLSSTPGIRWVVAFFRQFFSAVTKV
DYLTLRAGFINAHLSQNKFNDFHKYLIKRSMEDDFKVVFGISLPLWGYAITLEFLDIN
DWYLFFIHLTLEQNAFQMAHFWWTVAFFGLKKOYHQIGLSLFWVVVGLALQFICSYM
OWYLFFIHLTLEQNAFQMAHFWWTVAFFGLKKOYHQIGLSTMVVVGLALQFICSYM
TFPLXALVTQMGSNMKRSIFDEGTSKALTNWRMTAKEKKKVRDTDMLAMQMIGDATPS
RGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLNPN
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/tissue_type="leaf"
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/cultivar="Ingrid"
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Location/Qualifiers
                                                                                                              /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAB06083.1"
/db_xref="GI:1877221"
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            lnAsnSerLysPheAspPheHisLysTyrIleLysArgSerMetGluAsp 250
                                                                  GGCACCGAGGCCGAAGCCCAGCAAGTACGTTGACTACTGCCCGGAGGG
                                                                                              IleArgTrpValValAlaPhePheArgGlnPhePheArgSerValThrLy
                                       AAAACAGCAAGTTCGACTTCCACAAGTACATCAAGAGGTCGATGGAGGAC
eLeuThrLeuPheLeuAspIleAsnGlyValGlyThrLeuIleTrpIleS 284
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seq_documentation_block:
ID AAV35022 standard; DN
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AC AAV35022;
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DT 13-OCT-1998 (first e
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DT 13-OCT-1998 (first e
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KW Barley; MLO; mildew;
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KW Barley; MLO; mildew;
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KW Borley; MLO; mildew;
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KW Bo
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Database sequences: 1730436
Database length: 858457221
Search time (sec): 208.380000
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-Q-/cgn2_1/USPTO_spool/US09722377/runat_19072002_111536_29875/app_query.fasta_1.597
-Q-/cgn2_1/USPTO_spool/US09722377/runat_19072002_111536_29875/app_query.fasta_1.597
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                                                                                       Panstruga
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96GB-0015879.
96GB-0022626.
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                                                                                       ₽,
                                                                                           Schulzelefert PMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene.
                                                                                                                                                                          LTD JOHN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  out_format :
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of the MLO gene, wild-type Mlo exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of Mlo function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance especially resistance to powdery mildew or rust. The product can also be used for identifying compounds able to stimulate a defence response in a plant by interaction with encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1602 BP; 336 A; 488 C; 466 G; 312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 2; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Mlo gene of barley – used to develop products for the production of transgenic plants which have increased pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyThrGluGlyArgLysProSerLysTyrValAspTyrCysProGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rTrpAlaValAlaValValPheAlaAlaMetValLeuValSerValLeuM
                                                                                                                                                                                          ysTleCysIleSerGluAspAlaAlaAspValMetTrpProCysLysArg
                                                                                                                                                                                                                                                                                                                                                                                         GGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGACCCCATCATCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                      lGlyPheIleSerLeuLeuLleValThrGlnAspProIleIleAlaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGCCCTGTGGGAGGCGCTGGAGAAGATGAAGGCGGAGCTCATGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysAlaLeuTrpGluAlaLeuGluLysMetLysAlaGluLeuMetLeuVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTCGGACAAAAAAGGGGTGCCGGCGGGGGGGGCTGCCGGAGACGCCGTC
lePheValLeuAlaValPheHisValThrTyrSerValIleThrIleAla
                                                                                                                                                                                                                                                          GGCACCGAGGGCCGCAAGCCAGCAAGTACGTTGACTACTGCCCGGAGGG
                                                                                                                                                                                                                                                                                                                         AGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCCTGCAAGCGC
                                                                 CTAAGCCGTCTCAAAATGAGAACATGGAAGAAATGGGAGACAGAGACCAC
                                                                                LeuSerArgLeuLysMetArgThrTrpLysLysTrpGluThrGluThrTh
                                                                                                                                 TCTTCGTGCTCGCGGTCTTCCATGTCACCTACAGCGTCATCACCATAGCT
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Gaps: 0
Percent Identity: 100.000
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1401 TCACAAGGGCATGGGGCGGTCGGACGACCCCAGAGCGCGCCCACCTCGC 1450
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                                                                                                                                                                                                                                                                                                                                                                                                                CTACCACACGCAGATCGGGCTGAGCATCATGAAGGTGGTGGTGGGGGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roAspTrpValLeuPhePheIleHisLeuThrLeuPheGlnAsnAlaPhe 350
                                                                                  ArgGlySerSerProMetProSerArgGlySerSerProValHisLeuLe 467
                                                                                                                                                                                                                                                                         STyrHisThrGlnIleGlyLeuSerIleMetLySValValValGlyLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGACTGGGTCCTTCTTCATACACCTGACGTTGTTCCAGAACGCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $GlyAlaProValValGluProSerAsnLysPhePheTrpPheHisArgP|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCATCATGAGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCGTCATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTTCATCCCTCTCGTGATCCTCTTGTGTGTTGGAACCAAGCTGGAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCACCCTCTTCCTTGACATCAATGGGGTTGGCACGCTCATCTGGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eLeuThrLeuPheLeuAspIleAsnGlyValGlyThrLeuIleTrpIleS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspPheLysValValValGlyIleSerLeuProLeuTrpGlyValAlaII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lnAsnSerLysPheAspPheHisLysTyrIleLysArgSerMetGluAsp 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sValAspTyrLeuThrLeuArgAlaGlyPheIleAsnAlaHisLeuSerG
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                                                                                                                                                                                                                         rLysAlaLeuThrAsnTrpArgAsnThrAlaLysGluLysLysLysValA 434
                                                                                                                                                                                                                                                                                                                                             CTCTCCAGTTCCTCTGCAGCTATATGACCTTCCCCCCTCTACGCGCTCGTC
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                               uHisLysGlyMetGlyArgSerAspAspProGlnSerAlaProThrSerP 484
                                                                                                                                      GAGACACGGACATGCTGATGGCTCAGATGATCGGCGACGCAACACCGAGC
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1

alignment\_scores:
 Quality:

Sequence 1917 BP;

395 A; 575 C; 554 G; 393 T; 0 other;

Percent Similarity:

Ratio:

432.00 0.812 99.812

Percent Identity:

99.812 533

Length:

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seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
                  The sequence is that of the MIO gene, wild-type MIO exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of MIO function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance especially resistance to powdery mildew or rust. The product can also be used for identifying compounds able to stimulate a defence response in a plant by interaction with encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-1998
                                                                                                                                                        New isolated Mlo gene of barley - used to develop products for the production of transgenic plants which have increased pathogen
                                                                                                                                                                                                                           Bueschges R,
                                                                                                                                                                                                                                                                                                                                                                                                 polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare MLO gene.
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                                                                                                                         Disclosure; Fig
                                                                                                                                                                                                                                                 (INNE-) INNES
                                                                                                                                                                                                                                                                        29-JUL-1996;
30-OCT-1996;
                                                                                                                                                                                                                                                                                             07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                WO9804586-A2
                                                                                                                                                                                          1998-159149/14.
DB; AAW59443.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                  CENT INNOVATIONS LTD JOHN.
                                                                                                                                                                                                                           Panstruga
                                                                                                                                                                                                                                                                      97GB-0004789.
96GB-0015879.
96GB-0022626.
                                                                                                                                                                                                                                                                                                                                                                                        /product= MIO protein
1890..1895
/*tar-
                                                                                                                                                                                                                                                                                                                    97WO-GB02046
                                                                                                                         7; 150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
225..1826
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                                                                                                                                                                                                                            Schulzelefert PMJ
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alignment_block:
US-09-722-377-1 x AAV35026
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575
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                                                                                                                                                                                                                                                                                                                   isGlnThrSerPheValLysArgHisLeuGlyLeuSerSerThrProGly 200
                                                                                                                                                                                        lGlyPheIleSerLeuLeuLeuIleValThrGlnAspProIleIleAlaL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTCGTGCTCGCGGTCTTCCATGTCACCTACAGCGTCATCACCATAGCT
                                                                                                                                                                                                                       CTAAGCCGTCTCAAAATGAGAACATGGAAGAAATGGGAGACAGAGACCAC
                                                                                                                                                                                                                                                                                                                                                                                GGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGACCCCCATCATCGCCA 474
                                GACTICAAGGICGICGCCATCAGCCTCCCGCTGTGGGGGTGTGGCGAT 1024
                                       AspPheLysValValValGlyIleSerLeuProLeuTrpGlyValAlaII 267
                                                                                                                                                                                                                                                                                                                                                                                                               424
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                                                             974
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517	501	484	467	451	434	417	401	384	367	351	334	317	301	284
1775	1725	1675	1625	1575	1525	1475	1425	1375	1325	1275	1225	1175	1125	1075
rAlaLeuGluAlaAspIleProSerAlaAspPheSerPheSerGlnGly 5	ProValHisArgLeuAsnProAsnAspArgArgArgSerAlaSerSerSe 	roArgThrGlnGlnAlaArgAspMetTyrProValValValAlaHis	UHISLYSG1YMetG1YArgSerAspAspProGlnSerAlaProThrSerP	ArgGlySerSerProMetProSerArgGlySerSerProValHisLeuLe	rgAspThrAspMetLeuMetAlaGlnMetIleGlyAspAlaThrProSer	rLysalaLeuThrasnTrpargasnThralaLysGluLysLysLysLysVala	ThrGlnMetGlySerAsnMetLysArgSerIlePheAspGluGlnThrSe	laLeuGlnPheLeuCysSerTyrMetThrPheProLeuTyrAlaLeuVal (	STYTHISTHTG1nI1eGlyLeuSerTleMetLysValValValGlyLeuA:	GlnMetAlaHisPheValTrpThrValAlaThrProGlyLeuLysLysCy:	roAspTrpValleuPhePheIleHisLeuThrLeuPheGlnAsnAlaPhe:	SG1yAlaProValValGluProSerAsnLysPhePheTrpPheHisArgP:	IleIleMetGluMetAlaLeuGluIleGlnAspArgAlaSerValIleLy :	erPheIleProLeuVallleLeuLeuCysValGlyThrLysLeuGluMet : 
33	517	500	484	467	450	434	417	400	384	367	350	334	317	300
823	1774	1724	1674	1624	1574	1524	1474	1424	1374	1324	1274	1224	1174	1124

AAV35022
IID AAV3
XX
XX
AC AAV3
AC AAV3
AC AAV3
AC BAV1
13-C
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DE HOIC
XX
KW BAI1
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YW99

Hordeum vulgare.

/\*tag= a /product= MLO protein Location/Qualifiers Barley; MLO; mildew; pathogen; resistance;

SS

13-OCT-1998 AAV35022;

(first entry)

Hordeum vulgare cv. Ingrid

MLO gene.

AAV35022 standard; DNA; 1602 BP.

ΧX

05-FEB-1998 WO9804586-A2

29-JUL-1997;

97WO-GB02046

07-MAR-1997; 29-JUL-1996; 30-OCT-1996;

97GB-0004789. 96GB-0015879. 96GB-0022626.

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which have increased patho;

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The sequence is that of the MIO gene, wild-type MIO exerts a n regulatory function on a pathogen defence response, such that exhibit a defence response in the absence of pathogen. Down-r or out-competition of MIO function may be used to stimulate a response in transgenic plants conferring increased pathogen re especially resistance to powdery mildew or rust. The product c be used for identifying compounds able to stimulate a defence in a plant by interaction with encoded polypeptide.

pathogen resistance, product can

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also

Down-regulation a negative

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Sequence

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New isolated Mio gene of barley - used to develop products for the production of transgenic plants which have increased pathogen resistance % \left( 1\right) =\left\{ 1\right\}
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Disclosure; Fig 6; 150pp; English.

The sequence is that of a homologue of the MLO gene, wild-type Mlo exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of Mlo function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance, especially resistance to powdery mildew or rust. The product can also be used for identifying compounds able to stimulate a defence response in a plant by interaction with encoded polypeptide.

Sequence 2425 BP; 525 A; 692 C; 596 G; 612 T; 0 other;

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acctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcacccg
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 Mismatches

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Search completed: July 23, 2002, 13:30:22 Job time: 6946 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Panstruga, R. and Bueschges, R.

POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-JAN-1997) Panstruga R., John Laboratory, Colney Lane, Norwich, Norfolk, Location/Qualifiers
1, 1917
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Direct Submission
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                                                                                                              100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                     /protein_id="Cab06083.1"
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//db_xref="GI:1877221"
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FQHRHKKALWEBLEKMARELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGT
EGRKPSKYVDYCPEGKVALMSTGSLHOLHVEIFVLAVFHYTYSVLTIALSRLKMETWK
KWETETTSLEVGFANDPARFRFITHOTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKV
DYLTLARGFINAHLSQNSKFDDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLELDING
VGTLIWISFIPLVILLCVGTKLEMIINEMALEIQDRASVIKGAPVVEPSNKFFWFHRP
DWVLFFIHLTLEQNAKENSIFDEDTSKALTNWRNTAKEKKKVRDTMLMAQMIGDATPS
TEPLYALVTQNGSMAKENSIFDEDTSKALTNWRNTAKEKKKVRDTMLMAQMIGDATPS
RGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVAHPVHRLNPN
DRRRSASSALEADIPSADFSFSQG"
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/product="Mlo"
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acgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggtg
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Eukaryota; Viridiplantae; Strept

Spermatophyta; Magnoliophyta; Li

Pooldeae; Triticeae; Triticum.

1 (bases 1 to 513)

Hu,D., Xie,W. and Zhao,G.
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                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                           Submitted (12-MAY-2000) Biotechnology Institute, University, 268 Kuaixuan Rd., Hangzhou, Zhejiang
                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                          Xie,W.
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/protein_id="Ak58574.1"
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ANDPARERETHOTSEVKRHLGLSSTPGIRMVVAFERQEFRSVTKYDILTLRAGFINAH
LSQNSKFDFHKYIKRSWEDDFKVVVGISLPLWGVAILTLFHDINGVGTLIWISFIPLV
ILLCVGTKLEM"
                                                                                                    /organism="Triticum aes
/cultivar="Huixianhong"
/db_xref="taxon:4565"
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yta; Liliopsida; Poales; Poaceae;
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Query Match Best Local Sin Matches 511;

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Score 411; DB 8; Pred. No. 1.1e-211; 0; Mismatches 2;

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Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Pooideae; Triticeae; Hordeum.

(bases 1 to 2431)
Panstruga,R. and Bueschges,R.
POLYNUCLEOTIDE AND ITS USE FOR MODULATING
                                                                                                                                                                                                                                                                                                               Sequence 5 from A92831
                                                                                                                                                                                      Patent: WO 9804586-A 5 05-FEB-1998;
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llarity 100.0%;
Conservative
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/organism="Hordeum vulgare"
/db_xref="taxon:4513"
/clone="MLO"
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Hordeum vulgare I
Y14573
Y14573.1 GI:2894
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barley.
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                                                                                                                                                                                                                                          Direct Submission
Submitted (12-AUG-1997) R. Panstruga,
Innes Centre, Colney Norwich NR4 7UH,
Related entry: Z83834.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare
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nstruga,R.
                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 59748)
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'gene-Mio'

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/note="putative (+) strand"

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## ALIGNMENTS

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1 (bases 1 to 1602)

Panstruga, R. and Bueschges, R.

POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
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/organism="Hordeum vulgare"
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1 (bases 1 to 1917)
Panstruga, R. and Bueschges, R.
POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE H
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Mlo gene.
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Submitted (09-JAN-1997) Panstruga
Laboratory, Colney Lane, Norwich,
Location/Qualifiers
                                                                                                                                                                           Bueschges,R., Hollricher,K.,
Frijters,A., van Daelen,R.,
Groenendijk,J., Toepsch,S.,
Schulze-Lefert,P.
The barley Mlo gene: a novel
                                                                                                                           2 (bases 1 to 1917)
Panstruga, R.
                                                                                                                                                           resistance
Cell 88 (5
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Spermatophyta; Magnoliophyta; Liliopsida;
Pooideae; Triticeae; Hordeum.
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1. 1917
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and 3'-RACE"
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Vos,P., Salamini,F. and
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Norfolk,
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vgtltwisfiplvillcvgtklemiimemaleiqdragyikgapvvepsnkfffwfhrp
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1868 bp Sequence 3 from Patent WO0078799.

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KKWETETASLEYQFANDPARFRETHQTSFVKRHLGLSSTFGVRWVVAFFRGFENSVIK
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VDYLTLRAGFINAHLSHNSKFDDEKXIKRSMEDDFKVVVGISLPLWCVAILTLFLDID
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DWYLFFIHLTLPQNAFOMAHFVWTVATPGLKKCFHMIGLSIMKVVLGHAQPLCSV
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ATCATCGTGTCCGTCCTCGTGGAGCACGCGCTCCATAAGCTCGGCCATTGGTTCCACAAG 167
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Submitted (16-MAR-2001) The Sainsbury Laboratory, John Innes
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VDYFTLRAGFINAHLSHNSKFDFHKYIKRSMEDDFKVVVGISLFLWCVALLTLFLDID
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ITFPLYALVTQMGSNMKRSIFDEQTAKALTNMRNTAKEKKVROTDMLMAQMIGDATP
SRGASPMPSRGSSPVHLLHKGMGRSDDPQSTPTSPRAMEEARDMYPVVVAHPVHRLNP
ADRRSYFSSALDVDLFSADFSFSQG"

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

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Yu,L., Niu,J.-S., Ma,Z.-Q.,
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                         Yu, L., Niu, J.-S., Ma, Z.-Q., Cloning, location and expres
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ttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggc
                            TCGTTCGTGAAGCGGCACCTGGGCCTGTCCAGCACCCCGGCGTCAGATGGGTGGTGGCC
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/protein id="AAK60566.1"
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/db_xref="qi:14334167"
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/translation="MAKDDGYPPARTIPETPSWAVALVFAVMIIVSVLLEHALHKLGH
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KKWETTASLEYQFANDPARFRETHQTSFVKRHIGLSSTPGVRWVVAFFROFFRSVTK
VDYLLTAGFINAHLSQNSKFDFHKIIKRSMEDDFKVVVGISLFLWAVALILTLFLDID
GIGTLTWVSFIPLIILLCVGTKLEMIIMMALEIQDRSSVIKAPVVVEPSNKFFWFHR
PDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKDCFHMNIGLSIMKVVLGLALQFLCSY
ITFFLYALVTGMGSNNKRSIFDEQTAKALTNWRNTAKEKKVRDTDMLWAQMIGDATP
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/chromosome="2A; 2B; 2D"
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Kramer, C.M., Wan Patton, D.A. and

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Elliott, C.E. and Sch
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79; Conservative
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                                                                                                                                                                                                                                                                                                324
                                                                                                                                                                                                                                                                                         /product="seven transmembrane-spanning protein"
/product="seven transmembrane-spanning protein"
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/db_xref="G1:15290591"
/db_xref="G1:15290591"
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SlplkavalifileLDIDGIGTLTWVSF1PLIILLCVGTKLEMIIMEMALEIQDRSSVI
SLPLKAVAILTLELDIDGIGTLTWVSF1PLIILLCVGTKLEMIIMEMALEIQDRSSVI
SLPLKAVAILTLELDIDGIGTLTWVSF1PLIILTFQNAFQMAHFVWTVATPGLKCOFHMNIGL
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SLPKAVAILTLELDIDGIGTSUFFSUFFSUFFSUFFX
KGAPVVEPSNKFFWFHREDWVLFFIHLTLFQNAFGMAHFVWTVALTMRANTAKEKK
VRDTDMLMAQMIGDATPSKGTSSWPSKGSSPVHLLOKGWKRSDDPQSAPTSPRTMEEA
RDMYPVVVAHPVHRLNPADRRRSVSSSALDADIPSADFSFSQG"
24 a 407 c 374 g 294 t
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<1. .1399
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/codon_start=1
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/cultivar="Bob White"
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                                     ggaggctagggacatgtacccggttgtggtggcgcacccggtgcacagactaaatcctaa
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1272; Conserv
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                                     TGGCAAAGGCAAAGGACAATCACCGGAGGCTTCTCTGGCTCCAAGGCGAGAGCGAGACCCA
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CCACGTCTTGTACAGCGTCGTCACCATGACCCTAAGCCGTCTCAAAATGAAGCAATGGAA
         ccatgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaa
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A92838
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Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 1635)
Panstruga_R. and Bueschges_R.
Pollynucleotide and ITS USE FOR MODULATING
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INNES JOHN CENTRE INNOV LTD (GB); PA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
/db_xref="taxon:4513"
/clone="MLO HOMOLOGUE"
, 496 c 520 g 304 t
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Pred. No. 2.2e-149;
0; Mismatches 270;
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          cccggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcga 1559
                                                               GCCGCAGATGGGCGCCGCCGACGCCGAGCGTCGGCTCGTCGCCG-------
TCCGGCGCGAAGGTACCTCCTTGTGACGGGTGGAGGTCGGCCTCGTCGCCGGCGCGCTCGA 1589
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Elliott,C. and Schulze-Lefert,P.
Direct Submission
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Oryza sativa Mlo (Mlo) mRNA,
AF388195
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Kim,M.C., Lee,S.H., Kim,J.K., Chun,H.J., Kim,J.C., Heo,W.D., Chung,W.S., Choi,M.S., Park,C.Y., Yoon,H.W. and Cho,M.J. Isolation and characterization of Mlo homolog in rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                 1 (bases 1 to 1872)

Briggs, S.P. and Simmons, C.R.

Manipulation of mlo genes to enhance disease resists

Patent: PCT WO/00/01722-B 07-JUL-1999;

Cahoon, R.E., Miao, G.-H., Rafalski, J.A. and Taramino,
Zea mays cDNA encoding southern corn leaf blight res
Patent: PCT W09923235-B 05-NOV-1999;

3 (bases 1 to 1872)

Bevoto, A., Hartmann, A., Piffanelli, P., Elliott, C., S
Taramino, G., Goh, C.-S., Cohen, F.E., Schulze-Lefert,
Panstring P.
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Zea mays
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Panstruga, R.
Molecular phylogeny and domain-specific co-evolution
plant-specific seven transmembrane Mlo family
Unpublished
4 (bases 1 to 1872)
                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; El
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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Cohen,F.E., Schulze-Lefert,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simmons, C.R., Taramino, G. and Powell, W.
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EPQSGPASFGRELGDMYPVADGHRLHRLDPERWRPASSTAVNIDIADADFSFSMR"
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Qy 1544 cytcytcygccttcyaayccyacatccccaytycayatttttccttcayc 1593	Qy 1484 cggttgtggtggcgcacccggtgcacagactaaatcctaacgacaggaggaggaggtccgcct 1543	acyacoccagagogogoccacoccoccaagyaggacallallallallallallallallallallallallal	1364 cgatgccgagccggggctcatcacccgtgcacctgcttcacaagggcatgggcggtcgg   1	Qy 1304 acacggacatgctgatggctcagatgatcggcgcaacaccgagccgaggctcgtcgc 1363	Qy 1244 agacgtccaaggcgctcaccaactggcggaacacggccaaggagaagaagaaagtccgag 1303 	Qy 1184 ccctctacgcgctcgtcacacagatgggatcaaacatgaagaggtccatcttcgacgagc 1243	Qy 1124 gcatcatgaaggtggtggtggtgggctatacttccagttcctctgcagctatatgaccttcc 1183	Qy 1064 ttgtgtggacagtggccacgcccggcttgaagaaatgctaccacacgcagatcgggctga 1123	Qy 1004 actgggtcctcttcttcatacacctgacgttgttccagaacgcgttttcagatggcgcatt 1063	Oy 944 tcatcaagggggccccgtggtcgagcccagcaacaagttcttctggttccaccgccccg 1003	Oy 884 gaaccaagctggagatgatcatcatggagatggccctggagatccagggccgggcgagcg 943	Oy 824 atggggttggcacgctcatctggatttctttcatccctctcgtgatcctctttgtgtgttg 883	Oy 764 tcgtcggcatcagcctcccgctgtggggtgtggcgatcctcaccctcttccttgacatca 823	Qy 704 acagcaagttcgacttccacaagtacatcaagaggtcgatggatg	Qy 644 tcaccaaggtggactacctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaa 703 	Qy 584 totocagcaccoctggcatcagatgggtggtggccttcttcaggcagttcttcaggtcag 643		491

Search completed: July 23, 2002, 09:37:03 Job time: 2196 sec

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## ALIGNMENTS

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186 TSFVKRHLGLSSTÞGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIK 245	126 SLHQLHVEIFYLAVEHYTYSVITIALSRLKMITWKKWETETTSLEXQFANDPARFRETHQ 185 	GFISLLLAVTQDP-ISGICISQKAASIMRPCK-VEPGSVKSKYKDYYCAKEGKVALMSTG	68 GFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVALMSTG 125	9 PARTLPETPSWAVALVFAVMIIVSVLLEHALHKLGHWFHKRHKNALABALEKWKAELMLV 68	8 PARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWEQHRHKKALMEALEKMKAELMLV 67	hes 469; Conservative 22; Mi	Watch 87.3%;	SEQUENCE 534 AA; 60298 MW; 6C9640F30FDE5189 CRC64;	EMBL; AF384144; AAK60566.1;		"Cloning, location and expression of MLo gene from wheat.";	Yu L., Niu JS., Ma ZQ., Chen PD., Liu DJ.;	SEQUENCE FROM N.A.	[1]	NORT TRANSFORM	spermatopnyta; wagnotiopnyta; הונוסטינומ; Poates; Poacede; Pootdede; mriticeae; אינונים אינונ	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Triticum aestivum (Wheat).		(TrEMBLrel. 19, Last	(TrEMBLicel, 19,	Ol-DRC-2001 (MrEMBirel 19. Created)	Q94F72 PRELIMINARY; PRT; 534 AA.	77 1 72
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Q94FR4;
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Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SEVEN TRANSMEMBRANE-SPANNING PROTEIN.
MLO2.
                                                                                                                                                                                                                                                                                                                                                                        Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C., Taramino G., Goh C.-S., Schulze-Lefert P., Panstruga R.; "Co-Evolution among intracellular domains and the C-terminus oseven-transmembrane Mlo protein is suggested by a detailed computational analysis.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Triticum aestivum (Wheat).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticeae; Triticum.
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                                                                                                                   LMSTGSLHQLHVF1FVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
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 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM
                              RFTHQTSFVKRHLGLSSTPGVRWVVAFFRQFFRSVTKVDYFTLRAGFINAHLSHNSKFDF
                                                        RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
                                                                                      LMSTGSLHQLHIFIFVLAVFHVTYSVIIMALSRLKMRTWKKWETETASLEYQFANDPARF 181
                                                                                                                                                   ELMLVGFISLLLAVTQDP-ISGICISEKAASIMRPCKL-PPGSVKSKYKDYYCAKQGKVS
                                                                                                                                                                 ELMLVGFISLLLIVTQDFIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVA 120
                                                                                                                                                                                                             DDEYPPARTLPETPSWAVALVFAVMIIVSVLLEHALHKLGHWFHKRHKNALAEALEKIKA 63
                                                                                                                                                                                                                                         DKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKA 62
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88.0%;
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Q94F71;
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
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SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF384145; AAK60567.1; -.
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YU L., Niu J.-S., Ma Z.-Q., Chen P.-D.,
"Cloning, characterization analysis and
wheat.";
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NCE 534 AA;
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87.6%;
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Last sequence update)
Last annotation update)
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Pred. No. 5.2e-223;
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a; Poales; Poaceae; Pooidea
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Spermatophyta; Wagnollophyta; Lillopsida; Poales; Poaceae; Pooideae;
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DIPSADFSFSQG 533
                                                                                                 SPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEA 521
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                                                              SPVHLLQKGMGRSDDPQSAPTSPRTMEEARDMYPVVVAHPVHRLNPADRRRSVSSSALDA
                                                                                                                                                                                            QMGSNMKRSIFDEQTAKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGTSPMPSRGS
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397; Conserv
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 3,
clone:P0043E01.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP000615; BAA85400.1; -.
InterPro; IPR004326; Mlo.
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Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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                                                              SASSSALEADIPSADFSFS
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF384030; AAK94907.1;
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O1-DEC-2001 (TrEMBLrel. 19,
O1-DEC-2001 (TrEMBLrel. 19,
O1-DEC-2001 (TrEMBLrel. 19,
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STRAIN=CV. IR64; TISSUE=LEAF;
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                                                                                                                                                                                                                                       VDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGV
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AASSSAIQVDIADSDFSFS
                           SASSSALEADIPSADFSFS 531
                                                                               SRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVA-----HPVHRLNPNDRRR
                                                                                                                         LFFIHLILFQNAFQMAHFVWTLATPGLKKCFHENWGLSIMKVVVGIFIQFLCSYSTEPLY
                                                                                                                                                                                              LFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLY 397
                                                                                                                                                                                                                         GTLIWISEVPLVILMLVGTKLEMVIMEMAQEIQDRATVIKGAPVVEPSNKYFWFNRPDWV
                                                                                                                                                                                                                                                                                 VDYLTMRQGFINAHLSQNSKFDFHKYIKRSLEDDFKVVVGISLPLMFVAILVLFLD1QGF
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                                                      SRGSSPVHLLHKQRVRSEDPPSAPASPGFAGEARDMYPVPVAPVVRPHGFNRTDP-DKRR
                                                                                                            ALVTQMGSNMKKTIFEEQTMKALMNWRKTAREKKKLRDADEFLAQMSGDTT---
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Pred. No. 5.9e-188;
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SEQUENCE 554 AA; 62454 MW; 029EAC3DBF80C847 CRC64;
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Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Lillopsida
Ehrhartoideae; Oryzeae; Oryza.
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                                     MAS---LSADIPDFDFSFS
                                                                                   SSRSASPVHLLQDHRARLDDPPSPITVASPPAPEE--DIYPVPAAAAFCQLLDDPPDRRW
                                                                                                         PSRGSSPVHLLHKGMGRSDDPQSAPT--SPRTQQEARDMYPVVVAHPVHRL--NPNDRRR 512
                                                                                                                                  YALVTQMGSNMKKTIFEEQTMKALMNWRKKAMEKKKVRDADAFLAQMSVDF-----ATPA 477
                                                                                                                                                YALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPM 456
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY079312; AAK38337.1; -.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Cahoon R.E., Mi
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ATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK--RG-----TEGRK----- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGRDLPSTPTWAVALVCAVIVLVSVAMEHGLHKLGHWFHTRQKKAMREALEKIKAELM 63
                                                 YMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDT----DMLMAQMIGD 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAEIM 65
                                YITFPLYALVTQMGSHMKKTIFEEQTAKAVMKWRKTAKDKVRQREAAGFLDVLTS---AD
                                                                                              FNRPGWVLFLIHLTALPERLPDGAFRLDTAHPRPEEMLPREAGLSIMKVAVGLVLQVLCS
                                                                                                                           FHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCS
                                                                                                                                                            LIDIKGFGTLVWISFVPLVILLLVGAKLEVVIMEMAKEIQDKATVIKGAPVVEPSDRFFW
                                                                                                                                                                                                                             FFASVTKVDYLTMRQGF1NYHLSPSTKFNFQQY1KRSLEDDFKVVVG1SLPLWFVA1FTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 AA; 63086 MW; B021C891063FF03B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andropogoneae;
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southern corn leaf blight resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1727; DB 10; Pred. No. 3.1e~157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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a; Poales; Poaceae; PACC cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
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Best Local Similarity
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Q94CG9;
01-DEC-2001 (TrembLrel. 19, C
01-DEC-2001 (TrembLrel. 19, I
01-DEC-2001 (TrembLrel. 19, I
SEVEN TRANSMEMBRANE PROTEIN M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.R., Taramino G., Goh C.-S., Cohen F.E., Schulze-Lefert P., Panstruga Molecular phylogeny and domain-specific co-evolution of the plan specific seven transmembrane Mio family.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY029317; AAK38342.1;
Transmembrane
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Cahoon R.E., Mia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Zea mays cDNA encoding
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                                                                                                                     189 VKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRS
                           248 MEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMAL
                                                                                                                                                                                                                                                                                                                      126 AVAVPGKKKKKAAAAADHLGGVVDWPPPYYAHNARMLAEASMATKCPEGKVPLISINALH
                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 LYGFISLLIVTQDPIIAKICISEDAADYMWPCK-----RGTE------
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                                                                                                                                                                                                      QLHIFIFFLAVFHVSYSAITMALGRAKIRAWKEWEKEAAGQDYEFSHDPTRFRFTHETSF
                                                                                                                                                                                                                                                        QLHVF1FVLAVFHVTYSV1T1ALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSF
                                                                                                                                                                                                                                                                                                                                                                                ----GRKPSK-----YVDY------
                                                                                                                                                                                                                                                                                                                                                                                                                                     VLGFISLLLVFGQNYII-KVCISNHAANTMLPCKLEAAAVEGKDGHGKEAAAVVAGKKKV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
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yta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
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Conthern corn leaf blight resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s; Score 1257; DB 10;
pred. No. 4.2e-112;
84; Mismatches 116;
Zea.
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Query Match
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Matches 25
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Q94KB3;
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MEMBRANE PROTEIN MLO12.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Esyermatophyta; Magnoliophyta; endicotyledons; core endicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
MCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Sim Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Pans "Molecular phylogeny and domain-specific co-evolution of specific seven transmembrane MLO family."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF369573; AAK53805.1; SEQUENCE 576 AA; 66548 MW; 43DA9F6AED64D8E6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                  VPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELML 66
                                                                                                                                                                                                                                                                                                           -----PSKYVDYCPE-GKVÄLMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMR
                                                                                                                                                                                                                                                                                                                                                                                     VGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTE------GRK-----
           PLYALVTOMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSS
                                                                                                     HGWDSYLWLPFLPLIVILIVGAKLQMIISKLGLRIQEKGDVVKGAPVVEPGDDLFWFGRP
                                                                                                                                                                                                                             TWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVVAFFRQFFRSVT
                                                                                                                                                                                                                                                                                              FYSPRRNLATKGYDKCAEKGKVALVSAYGIHQLHIFIFVLAVFHVLYCIITYALGKTKMK
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                                           RFILFLIHLVLFTNAFQLAFFVWSTYEFTLKNCFHKTEDIAIRITMGVLIQVLCSYITL
                                                               DWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTF
                                                                                                                         NGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWEHRP
                                                                                                                                                                                      KVDYLTLRAGFINAHLSQNS--KFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDI
                                                                                                                                                                        KVDYLTLRHGFIMAHLPAGSAARFDFQKYIERSLEQDFTVVVGISPLIWCIAVLFILTNT
Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1255.5; I
Pred. No. 6.7e-1
3; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9SXB6 PRELIMINARY; PRT; 573 AA.
Q9SXB6;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence up)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation)
T28P6.4 PROTEIN (MEMBRANE PROTEIN MLO2).
T28P6.4.
                                                                                                                                                                                                                                                                                                                                                                                                                   Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simu Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panst "Molecular phylogeny and domain-specific co-evolution of specific seven transmembrane MLO family.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC007259; AAD49991.1;

EMBL; AF369563; AAK53795.1;

EMBL; AF369563; AAK53795.1;

EMBL; DF3004.10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
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                                                                                                                                                                                                                                        KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSK-----
                                         VVAFFROFFRSVTKVDYLTLRAGFINAHLS--QNSKFDFHKYIKRSMEDDFKVVVGISLP
                                                                                               CIVTYAFGKIKMRTWKSWEEETKTIEYQYSNDPERFRFARDTSFGRRHLNFWSKTRVTLW
                                                                                                               DKPGRRLLLELAESYIHRRSLATKGYDKCAEKGKVAFVSAYGIHQLHIFIFVLAVVHVVY
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LWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPV
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                                                                                                                                                                                                                                                                                                                            261;
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61; Conservative
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Pred. No. 1e-11:
1; Mismatches
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eudicots; Rosid
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Liu S.,
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RESULT
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Q9SY94;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F. Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunni Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S. Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (APR-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005850; AAD25552.1; -.
InterPro; IPR004236; Mlo.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MADQ--VKEKTLEETSTWAVAVVCFVLLLISIVIEKLIHKIGSWFKKKNKKALYEALEKV 58
                                                                          FFROFFRSVTKVDYLTLRAGFINAHLSONS--KFDFHKYIKRSMEDDFKVVVVGISLPLWG
                                                                                                                                                        TYALGKTKMRRWKKWEEETKTIEYQYSHDPERFREARDTSFGRRHLSFWSKSTITLWIVC
                                                                                                                                                                                                   TIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIR-WVVA
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NCE 583 AA;
  VAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEP
                                                  FFRQFFRSVTKVDYLTLRHGFIMAHLAPGSDARFDFRKYIQRSLEEDFKTIVEINPVIWF
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67226
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Pred. No. 7.2e-1
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Liu S.,
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF369567; AAK53799.1;
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Matches 253; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E., Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; "Cryza sativa chromosome 10 BAC OSJNBb0064P21 genomic sequence."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC073166; AAG46114.1; ". CD263AD8F8C350FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; Ethiopsida; Poales; Tracheophyta; Ehrhartoideae; Oryzeae; Oryza, NCBI.TaxTha-4570.
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GDHFFWFGRPREILFLIHLVLFTNAFQLAFFVWSTYEFGLKNCFHESRVDVIIRISIGLL
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                                                                                                                                             LVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.8%; Score 1192; DB 10;
47.1%; Pred. No. 8.6e-106;
Live 80; Mismatches 146;
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Q94CH3;
Q94CH3;
Q1-DEC-2001 (TrembLrel. 19, C
01-DEC-2001 (TrembLrel. 19, L
01-DEC-2001 (TrembLrel. 19, L
SEVEN TRANSMEMBRANE PROTEIN M
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Briggs S.P., Simmons
"Manipulation of mlo
Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.R., Taramino G., Goh C.-S., Cohen F.E., Schulze-Leftert P., Panstruga "Molecular phylogeny and domain-specific co-evolution of the pla specific seven transmembrane Mlo family.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY(29313; AAK(38338.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cli
Panicoideae; Andropogoneae; Zea.
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NCBI_TaxID=4577;
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FQMAHEVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKR
                                        AHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLMGVAILTLFLDINGVGTLIWISFIPLV
                                                                                                                                                                                                             FS-CRKGMVSLVSADGMHQLHIFVFFLAVFHVTFSEFTMSLGRAKTRIWKVWEKETCSPQ
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                                                                                                AHLSPGTRF NFRKY I KRSLEDDFKTVVG I SPPLWASALAVML FNVHGWHNL FWFSA I PLV
                                                                                                                                                        YNYLNDPSKFRLTHQTSFVRQHASCWSKSTITLYFVSFFRQFFRSVRKTDYFTLRHGFIS
                                                                                                                                                                       VDYCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLE
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genes to enhance disease resistance in plants.";
to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                Score 1160; DB 10;
Pred. No. 9.9e-103;
1; Mismatches 174;
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Sear Job 1	Ор	Qy	망	ρ	DЪ	Qy	탕
Search completed: July 23, 2002, 14:32:55 Job time: 495 sec	526 DTERAEVRVNVVETAAAPSDVLQDSFSF 553	503 HRLNPNDRRRSASSSALEADIPSADFSF 530	SDTE	463PVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPV 502	1	410 SIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSS 462	360 FEITYFFWIWYEFGLRSCFHDNFEFIIARVCLGAIVQFMCSYITLPLYALVSQMGSEMKR 419

OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters:
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Copyright (c) 1993 - 2000 Comp
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080961 arabidopsis
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"A contiguous 60 kb genomic stretch from barley reveals molecular
evidence for gene islands in a monocot genome.";
Nucleic Acids Res. 26:1056-1062(1998).
-!- FUNCTION: MAY BE INVOLVED IN DOWN-REGULATING LEAF CELL DEATH AND
PATHOGEN DEFENSE FUNCTIONS.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- MISCELLANEOUS: REF.1 HAS SEQUENCED MLO IN STRAINS CV. CARLSBERG
-!- DIAMANT, CV. FOMA, CV. HAISA, CV. INGRID, CV. MALTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND MUTAGENESIS.
STRAIM-VARIOUS STRAIMS; TISSUE-Leaf;
MEDLINE-97207016; PubMed-9054509;
Bueschges R., Hollricher K., Panstruga R., Simons G., Wolter M.,
Frijters A., van Daelen R., van de Lee T., Diergaarde P.,
Groenendijk J., Toepsch S., Vos P., Salamini F., Schulze-Lefert P.;
"The barley Mlo gene: a novel control element of plant pathogen
resistance.":
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P93766;
Mendel; 13060; HORVU; 2260;1.
ITterPro; IPR004326; M10.
Pfam; PF03094; M10; 1.
Pransmembrane; Pathogenesis-related protein.
TRANSMEM 18 38 POTENTIAL.
TRANSMEM 63 83 POTENTIAL.
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
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15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                      EMBL; 283834; CAB06083.1; -. EMBL; Y14573; CAA74909.1; -.
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MEDLINE~98128007; PubMed~9461468;
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CYAA\_DICDI FML1\_GORGO 93.5 93.5 93.5

Y316\_MYCGE

Y306\_MYCPN

YD49\_THEMA

HSLU\_HELPY

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YHGE\_ECOLI

YML3\_ARATH

ML15\_ARATH

YML1\_ARATH MLO5\_ARATH

YML6\_ARATH MLH1\_ORYSA

YML2\_ARATH

ARATH

Minimum DB seq length: Maximum DB seq length:

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Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

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Perfect score:

US-09-722-377-1 2788

Post-processing: Minimum Match 0%

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R->W: IN MLO-9; CONFERS BROAD SPECTRUM
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V->E: IN MLO-13; CONFERS BROAD SPECTRUM
RESISTANCE TO POWDERY MILDEW FUNGUS.
S->F: IN MLO-17; CONFERS BROAD SPECTRUM
RESISTANCE TO POWDERY MILDEW FUNGUS.
W->R: IN MLO-1; CONFERS BROAD SPECTRUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Panstruga R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE MLO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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531
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305
423
60875
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69.58;
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POTENTIAL.
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Pred.
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No. 9
                                          VQHPARKVPPCDGWRSASSPALDAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .8e-156;
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049914;
15-JUL-1999
15-JUL-1999
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELDULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Panstruga R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004326; M
Pfam; PF03094; Mlo; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z95353; CAB08606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane
 351
                     300
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                                                                                     231
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                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                               ARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEAL - - - - EKMKAEL 64
                                                                                                                                                                                                                  MLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTE-----GRKPSKYV---DY 113
                                                                                                                                                                                                                                          SRELPETPTWAVAVVCAVLVLVSAAMEHGLHNLSH-----KTTAEVLIFLVLSALAEL 60
                                                              QFAIDPSRFRFTHQTSFVKRHLGSFSSTPGLRWIVAFFRQFFGSVTKVDYLTMRQGFINA
                                                                                                                     QFANDPARFRETHQTSFVKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINA
                                                                                                                                                      CSKFDGKVALMSAKSMHQLHIFIFVLAVFHVTYCIITMGLGRLKMKKWKKWESQTNSLEY
                                                                                                                                                                  CP--BGKVALMSTGSLHQLHVPIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEY 171
                                                                                                                                                                                               QMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRS
                     LLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAF
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38, Last sequence update)
38, Last annotation updat
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                                                                                                                                                                                                                                                                                               Score 1792; DB 1;
Pred. No. 3.4e-143;
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EE16772A9637416B CRC64;
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                                                                                                                                                                                                                                                                                                          Length 537;
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Matches 254; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nlerman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter T.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Hypothetical MLO-Like protein At2g39200.
AT2G33200 OR T16B24.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                 TRANSMEM
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                                                                                                                      TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                Hypothetical TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Integral membrane -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thaliana.";
Nature 402:761-768(1999).
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                                                                                                                                                                                                                                                                                                                   Pfam; PF03094; Mlo; 1.
                                                                                                                                                                                                                                                                                                                                                           EMBL; AC004697; AAC28997.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence and analysis of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C.;
                                                                                                                                                                                                                                                                                                                                          [nterPro;
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                                                                                                                 400
570
     Conservative
                                                                                                                                                                                                                                                                                       protein;
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176
293
323
377
                                                                                                                           65765
                         43.8%;
                                                                                                                                                                                                                                            Transmembrane.
4 POTENTIAL.
6 POTENTIAL.
                                                                                                                           MW.
          93;
                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
4C49FBF806F90910 CRC64;
                           Score 1220.5; DB Pred. No. 4.7e-95
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edons; core eudicots; Rosid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein (Potential).
          153;
                                                       DB 1;
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            Indels
                                                    Length
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dblyum T.V.,
                                                         570;
            61;
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            Gaps
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Venter J.C.;

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA;

STRAIN=CV. COLUMBIA;

STRAIN=CV. COLUMBIA;

MEDILINE-20083487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C. L., Barnstead M.E., Feldblyum Fuli C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Goodman H.M., Smerville C.R., Capenhaver G.P., Fraser C.M.,
                                                                                                                                                                                                 Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstrugg "Molecular phylogeny and domain-specific co-evolution of the plant-specific seven transmembrane MIO family."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
MLO-like protein 5 (AtMio5).
MLO5 OR AT2G33670 OR F4P9.44 OR T01B08.26.
                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                           LVGFISLLLIVTQDPIIAKICISEDAADVMWPC----KRGTEGRKP--SKYVD-----
GDIESASPANI - - -
                       ---RGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDM
                                                  STMKRSVFDDQTSKALKNWHKNAKKKSE-
                                                                                                   LFQNAFEITYFFWIWYEFGLRSCFHHHFALIIIRVALGVGVQFLCSYITLPLYALVTQMG
                                                                                                                            LFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMG
                                                                                                                                                      MIPPLITLAIGTKLQAIISDMALEIQERHAVIQGMPLVNVSDRHFWFSRPALVLHIIHFI
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                                                                                                                                                                                                                                                                              EYQFANDPARFRFTHQTSFVKRHLGLSSTPGIR-----WVVAFFRQFFRSVTKVDYLTLR
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16-OCT-2001 (Rel. 40, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Hypothetical MLO-11ke protein At2g17430
AT2G17430 OR F5J6.19
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Mlerman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter J.C.;
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SIMILARITY: BELONGS TO
                                                                                                                                                                   GAPSGGKELSQTPTWAVAVVCTFLILISHLLEKGLQRLANVCFLLLLLLELRVFLFKHSL
                                                                                                                                                                              FHIVYSLITMMLSRLKIRGWKKWEQETLSNDYEFSIDHSRLRLTHETSFVREHTSFWTTT
                             FHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SST
                                                                                                            SETYEFVSSQWLWKKHKNSLLEALEKIKAELMILGFISLLL-TFGEPYILKICVPRKAAL
                                                      SMLPCLSEDTVLFQKLAPSSLSRHLLAAGDTSINCKQGSEPLITLKGLHQLHILLFFLAI
                                                                                VMWPC-KRGT---EGRKPSKYVDY------
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39 59
62 8:
196 27
319 3:
346 3
346 3
580 AA;
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Pred. No. 1.3e
75; Mismatches
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                                                                       -CPEGKVALMSTGSLHQLHVFIFVLAV
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dblyum T.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
                                                                                                                                                                                                                             56;
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                                                                                                                                                                                                                            Gaps
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YML2_ARATH
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022757;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-MAR-2002 (Rel. 41, Last annotation update)
4 (Apothetical MLO-like protein At2g17480.
4 (Apothetical MLO-like protein A
                                           Hypothetical
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D. Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V. Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:761-768(1999).
-i- SUBCELLULAR LOCATION: Integral membrane
-i- SIMILARITY: BELONGS TO THE MLO FAMILY.
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TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                            EMBL; AC002329; AAB86524.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence and analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431
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                                                                                                                                                                                            PF03094; Mlo;
                                                                                                                                                                                                                     IPR004326; Mlo.
                      47
93
182
305
397
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                                                32
67
113
202
325
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     63247
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  ₩;
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     EAAA9CF15AA6AF49 CRC64;
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Score 1039;

DB 1;

Length 560;

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LOL_ARATH

ID MIOL_ARATH

ID MIOL_ARATH

ID MIOL_ARATH

ID MIOL_ARATH

STANGER

AC 049621; 022766;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-CCT-2001 (Rel. 40, Last annotation update)

DE MIO-1ike protein 1 (AtMIO!) (MIO protein homolog 1) (AtMIO-H1).

GN MIO1 OR MIO-H1 OR AT4G02600 OR T10P11.12.

GN MIO1 OR MIO-H1 OR AT4G02600 OR T10P11.12.

T1440psis thaliana (Mouse-ear cress).

Streptophyta; Embryophyta; Tracheophyta.

T-ae: Arabidopsis.
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Best Local
          MEDLINE=20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entlan K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Muelle
                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
   Kreis
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520
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   Ξ.
                                                                                                                                                       (MAY-1997)
 Delseny M.,
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Puigdomenech
                                                                                                                                                     the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DPETSDLDTDNEALTPPKSPPS---
Watson M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.7e-80
                                                                                                                                                                                                                                                            core eudicots; Rosidae,
 Schmidtheini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 106;
                Mueller M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470
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6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM

Matches Query Match Best Local

Similarity

33.4%;

Score 932.5; Pred. No. 7.

.4e-DB 1; 167;

526; 51;

Gaps

10;

Conservative

79;

Mismatches

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RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., Ra Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., Ra Hrishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Ra Ra Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., Ra Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., Ra Zaccaria P., Bevan M., Wilson R.K., Johnson E., Spiegel L., Schutz K., Huang E., Spiegel L., Ra Zechon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., Schott R., Johnson D., Ra Schneking T., Kalicki J., Graves T., Harmon G., Edwards J., Johnson D., Ra Kramer J., Fulton B., Miller N., Greco T., Kemp K., Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Ra Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L., Ra Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L., Ra Kramer J., Fulton J., Ryan E., Andrews S., Geisel C., Layman D., Ra Melson J., Spieth J., Ryan E., Andrews S., Gotton M., Joshu C., Ra Martie M., Stong C., Sun H., Lamar B., Yordan C., Ra Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ra Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Shah R., Swaby I.K., O'Shaughnessy A., Rol D., Shekher M., Matero A., Shah R., Ra Granat S., Shohdy N., Hasegawa R., Hameed A., Lodhi M., Johnson A., Chen E., Marra M., Mattienssen R., McCombie W.R.,
TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R. Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H., Dose S., de Haan M., Maarse A.C., Schaefer M., Meeller-Auer S., Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
                                                                                                                                            TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schnabl S., Hiller R., Johnson B., Casacuberta B., Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta B., Cibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Gibbons T., Weber N., Vandenbol M., Bargues M., Tacon D., Jesse T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reichert B., Portetelle D., Perez-Alonso M., Boutry M., E
Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
Langham S.-A., McCullagh B., Bilham L., Robben J.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandent
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandent
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R.,
                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:769-777(1999).
-I- SUBCELLULAR LOCATION: Integral membrane protein
-I- SIMILARITY: BELONGS TO THE MLO FAMILY.
                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weitzenegger I., Bothe G., Ramsperger U., Hilbert H., Braun M.,
Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
                                                                       TRANSMEM
                                                                                              TRANSMEM
                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                              Z95352; CAB08605.1; -AC002330; AAC78258.1; AL161494; CAB80753.1;
                                                                                                                                                                                                                                     IPR004326; Mlo.
                                                                                                                                                                                            Multigene
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82
181
308
329
393
  59126
                                                                                                                                                                                               family.
  MW;
                                                POTENTIAL.
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POTENTIAL.
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  8E63C276A71A9768 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herzl A.,
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15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
MLO-1ike protein 15 (AtMLO15).
MLO15 OR ATZG444110 OR F6E13.24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga "Molecular phylogeny and domain-specific co-evolution of the plant-specific seven transmembrane MIO family."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                STRAIN-CV. COLUMBIA;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.E., Feldblyum T.V.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Goodman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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  Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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                                                       "Sequence a
                                                                                                                 Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEHEWFSKPQIVLYLIHFILFQNAFEIAFFFWIWVTYGFDSCIMGQVRYIVPRLVIGVFI
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                                                                              and analysis of chromosome
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     LOCATION:
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     Integral membrane
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           (Potential)
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RESULT YML3\_AR

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YMI3\_ARATH STANDAKU;

YMI3\_ARATH STANDAKU;

0.23693;

15-JUL-1999 (Rel. 38, Created)

15-JUL-1999 (Rel. 38, Last sequence update)

11-JUL-1999 (Rel. 41, Last annotation update)

11-JUL-1999 (Rel. 41, Last annotation update)

11-JUL-1999 (Rel. 41, Last sequence update)

12-JUL-1999 (Rel. 38, Created)

13-JUL-1999 (Rel. 38, Created)

14-JUL-1999 (Rel. 38, Created)

15-JUL-1999 (Rel. 38, Created)

15-JUL-1999 (Rel. 38, Created)

16-JUL-1999 (Rel

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Best Local
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SEQUENCE
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Pfam; PF0;
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Transmembrane; Multigene family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGFIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEYTPTWVVALVCSVIVSISFAVERLIHRAGKHFKNNDQKQLFGALQKIKEELMLVGFIS
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AC004005; AAC23431.1;
Pro; IPR004326; Mlo.
                                               LHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAH 500
                                                                                                                                                   MKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHL
                                                                                                                                                                                                  PLILLAVGTKLEHIITDLAHEVAEKHIAVEGDLVVRPSDDLFWFQSPRLVLFLIHFILF
LGKGSSQQNQ-----
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418 P
56151 MW;
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Pred. No. 2e-70;
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          494
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-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE MLO FAMILY.
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155
                                                        244 IKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIM 303
                                                                                                                       118
                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                124 TGSLHQLHVF1FVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFT 183
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MVRTMEDEFHGIVGISWPLWVYAIVCICINVHGLNMYFWISFVPAILVMLVGTKLEHVVS 214
                                                                                                                                                                                                                                    YEGLEQLLRELEVLGITHVLYSGIAIGLAMSKL-----
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                                                                                                                                                                         HQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKY 243
                                                                                                                                                                                                                                                                                                                                                        -----TNQSSLPHHGIHEAS-----HQCGHGREPFVS 84
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PF03094; Mlo; 1.
Transmembrane.
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94
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183
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267
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27.2%;
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                                                                                                                   ----CFLRQFRGSIRKSDYFALRLGFLTKH-NLPFTYNFHMY 154
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Pred. No. 1.7e-34;
2; Mismatches 159
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80 A

65

342 HLTLFQNAFQMAHFVWTVATPGLKKCYH 369

282 WISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFI 341

WLPFIPLIIILVVGTKLQVIITQLGLSIQDRGDVVKGAPVVQPGDDLFWFGRPRLVLFLI

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SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
MLO-like protein (Fragment)
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P81785;
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                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases -!- SUBCELLULAR LOCATION: Integral membrane protein (Pot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eurosids
                                                                                                                                                                                                                                                      Transmembrane.
                                                                                                                                                                                                                                                                     Pfam; PF03094; Mlo;
                                                                                                                                                                                                                                                                                                   EMBL; AJ005341; CAA06487.1; -.
                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McKay G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. ANTARES; TISSUE=Cotyledon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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    - I - SIMILARITY: BELONGS TO THE MLO FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 IDQAESIFGAAASSSSPQDGYTS-RVEEYLSETY 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 LHK-----GMGRSDDPQSAPTSPRTQQEARDMY 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 ESVRDSLHSWCKRVKERSKHTRSVCSLDTATIDERDEMTVGTLSRSSS-MTSLNQITINS 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 TFIWFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 KLALEVKEQQTGTSNGAQVKPRDGLFWFGKPEILLRLIQFIIFQMILIYFLLMQNAFEMA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 EMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVL-----FFIHLTLFQNAFQMA 353
                             224 RAGFINAHLS--QNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 HFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFD
 5 RYPIIAAHLAPGSESRFDFQKYVNRSLEDDFKVVVGISPILWFFAVLFLLSNTHGWVAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQTSKALTNWRNTAKEKKK-VRDTDMLMAQMIGD-----ATPSRGSSPMPSRGSSPVHL 466
                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I; Malpighiales; Linaceae; Linum.
                                                                                                                                                                                                                                                                                         IPR004326; Mlo.
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35
59 ·
119
217
217 AA;
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                 15.4%;
55.4%;
                                                                                                                                                    24604 MW; 4341CE37FC2E8493 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------FWCSYGTVPLNVIVTQMGSRHKKAVIA 307
                                                               23;
                                                                                 Score 429; DB 1;
Pred. No. 5.6e-29;
                                                                                                                                                                                                     POTENTIAL.
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                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane protein (Potential).
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                                                                                                 DB 1; Length 217;
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Matches 69
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_ECOLI
                                                                                                                                                                                                                                                                                                                                TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III. Bloch C.A., Perr
Riley M., Collado-Vides J., Glasner J.D., Rode C
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P45804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000415; AAC76427.1; -. EcoGene; EG12931; yhgE.
                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                       Hypothetical TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U18997; AAA58199.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                     TRANSMEM
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111 VDYCPEGKVALMSTGSLHQLHVFIFVL-----AVFHV-----TYSVIT---
                                                                             64 KRIWGWIAIVFIATIGMSGWIKWQTDGMNPWRAEKAIWDFGCYLLLMAMLLLPWIQQSLR
                                                                                                                       4 VELSPATRWGMIATGLLQGLVCYLLIAWLSGKNHSWIVYGVPATVAFSSVLLFSVISFKQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: SOME, TO B.SUBTILIS YRDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFCLFQNAFQLAFFIWSVYEFGIKTCFH 152
                                                        FANDPARERFTHQTSF--VKRHLGLSSTPGIRWVV-----
                                 IRNDSSRYRYFYQSVWHNVLILLVIFLANGLTWLVLLLWSELFKLVGITFFNTLFFATDW
                                                                                                    -----IALSRLKMRTWKKWETETTS----
                                                                                                                                                                                 Similarity
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(Rel. 32,
(Rel. 40,
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                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                 protein;
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268
306
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19.7%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                             MW;
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                                                                                                                                                                                Score 102.5; D
Pred. No. 0.61;
                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                             529E33C38D5BEF59 CRC64;
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions ng as its content is in
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Rode C.K., Mayhew G.F.
Goeden M.A., Rose D.J.,
                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                      ; 68
                                                                                                                                                                                                                                                                                                                                                                   proteome
                                                        -----AFFRQFFRSVTK 217
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                                                                                                                                                                                            Length
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RESULT 13
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Q9ZLW1;
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Alm R.A., Ling L. S.L., Moir D.T., King B.L., Brown E.D., Smith D.R., Noonan B., Guild B.C., deJOnge B.L., Carmel G. Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., IV Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Trust T.J.;
                                                                                                                                                                                                      Chaperone; ATP-binding; Complete proteome.
NP_BIND 59 66 ATP (POTENTIAL)
SEQUENCE 443 AA; 50164 MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
ATP-dependent hsl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEX (BY SIMILARITY).
-!- SUBUNIT: INTERACTS WITH HSLV (BY SIMILARITY)
-!- SUBCELLULAR LOCATION: OFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic sequence comparison of two unrelated gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                          Pfam; PF00004; AAA; 1
PRINTS; PR00300; CLPF
SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSLU OR JHP0465.

    -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
    -!- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter
                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001480; AAD06034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                         HSSP; P32168; 1D02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 FIYLTL--GLVTALAVILARTQSRLID-----SIQKLFTLIATGLLPL--VSLLTLMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6-OCT-2001
256 E---IDKIAVSSKEGSRQDPSKEGVQR------DLLPIVEGSVVNTKYGSIKTEHILFI 305
                                                                196
                              78
                                                                                    34 MEHGLHKLGHWFQHRHKKAL--WEALEKMKAEL---MLVGFI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPLRCLIKTALLVAPLYVFV----AAWALW-----LRVAQYGWTV
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                            QDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCP--EGKVALMSTGSLHQLHVFIF 135
                                                                VQENLIKVFHKEQDKVKKTLSVKEAKEALKAEISDTLLDGEAIKMEGLKRAESSGVIFID 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTV 359
                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                        IPR003959; AAA_subfam.
IPR001270; CLP_AB.
                                                                                                                                                                                                                                                                                                                                          IPR003593; AAA.
                                                                                                                                Conservative
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40, Last
40, Last
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40, Last annotation update)
protease ATP-binding subunit
                                                                                                                                              3.4%;
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                                                                                                                                35;
                                                                                                                                              Score 95.5;
Pred. No. 1
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                                                                                                -SLLLIVT
                                                                                                                                59;
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RESULT PROCESS OF THE PROCESS OF THE
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Query Match
Best Local Similarity
                                                                                                           PROSITE; PS00349; CTF_NFI; 1.

Transcription regulation; DNA replication; DNA-binding; Activator; Nuclear protein; Multigene family; Alternative splicing.

DOMAIN

68 176 DWA.

SEQUENCE 506 AA; 55461 MW; 6315A9474807F4C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 28:8191-8200(1989).

1: FUNCTION: RECOGNIZES AND BINDS THE PALINDROMIC SEQUENCE 5'-
TIGGCUNUNUNGCCAA-3' PRESENT IN VIRAL AND CELLULAR PROMOTERS AND IN
THE ORIGIN OF REPLICATION OF ADENOVIRUS TYPE 2. THESE PROTEINS ARE
INDIVIDUALLY CAPABLE OF ACTIVATING TRANSCRIPTION AND REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Nuclear factor 1 C-type (Nuclear factor 1/C) (NFI-C) (NFI-C) (NF-I/C)
(CCAAT-box binding transcription factor) (CTF) (TGGCA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winnacker E.L.; "Structural and functional organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-90105327; PubMed-2513876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823;
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IPR000647; CTF_NFI.
IPR003619; Dwarfin_A.
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MEDLINE-99287316; PubMed=10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

MCDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Fridence for lateral gene transfer between Archaea and Bacteria fromme sequence of Thermotoga maritima.";

Nature 399:323-329(1999).

1- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY.
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16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=MSB8 / DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Thermotogales; NCBI_TaxID=2336;
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                                                                                                                                                     TIGR;
                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                     306 ALEIQDRASVI-----KGAPVVEP 324
                                                                                               122 MSTGSLHQLHVFIFVLA------VFHVTYSVITIALSRLKMRTWKKW------ 162
                                                                                                                                                                                        121 DKIMNELEPKLTDELNYVESLYTTNE-VSVTTIIVETLEGLGYTVEYIREIASEFYLIYP 179
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-09-183-959-6
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US-09-245-041-15
PCT-US94-00198-4
US-08-050-684-2
US-08-050-684-2
US-08-050-684-2
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US-08-444-1018-70
US-08-444-1018-70
US-08-444-1018-42
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US-08-714-524D-44
US-08-718-2311-2
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361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL

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Db 61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMMPCKRGTEGKRSKYVDYCPEGKV.  Qy 121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKHRTWKKWETETTSLEYQFANDPAR	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 2.9e-294; Best Local Similarity 100.0%; Pred. No. 2.9e-294; Matches 533; Conservative 0; Mismatches 0; Indels 0; G  NSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM Db 1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM	RESULT 1 US-09-350-268-3 (Sequence 3, Application US/09350268 (Sequence 3, Application US/09350268 (Patent No. 621143) (Patent	75 2.7 602 4 US-09-303-069-16 ALIGNMENTS	28 77 2.8 2188 4 US-09-404-650-4 Sec 29 76.5 2.7 350 5 PCT-US93-08528-41 Sec 31 76.5 2.7 473 1 US-08-439-131A-4 Sec 31 76.5 2.7 473 1 US-08-49-99-004-5 Sec 32 76.5 2.7 473 1 US-08-69-99-004-5 Sec 33 76.5 2.7 473 1 US-08-69-99-004-5 Sec 34 76.5 2.7 1440 4 US-09-357-251-37 Sec 35 76 2.7 318 1 US-08-69-286-10 Sec 36 75.5 2.7 782 4 US-09-469-253-10 Sec 39 75.5 2.7 782 4 US-09-469-253-10 Sec 39 75.5 2.7 782 4 US-09-469-253-10 Sec 39 75.5 2.7 782 4 US-09-642-146-10 Sec 39 75.5 2.7 430 2 US-08-931-047-2 Sec 42 75 2.7 430 2 US-08-931-047-2 Sec 42 75 2.7 430 2 US-08-931-047-2 Sec 36 75 2.7 430 2 US-08-931-047-2 Sec 36 75 2.7 430 2 US-08-795-868-16 Sec 36 75 2.7 601 2 US-08-795-868-16 Sec 36 75 2.7 601 2 US-08-795-868-16 Sec 36 75 2.7 601 2 US-08-795-868-16 Sec 36 795-868-16 Sec 36 795
RKPSKYVDYCPBGKVA 120  RKPSKYVDYCPBGKVA 120  ETTSLEYQFANDPARF 180  ETTSLEYQFANDPARF 180  AGFINAHLSQNSKFDF 240	1 533;  0; Gaps 0;  (ALWEALEKM 60  (ALWEALEKM 60  DVCPEGKVA 120	Disease Resistance	16	Sequence 4, Appli Sequence 41, Appl Sequence 41, Appli Sequence 5, Appli Sequence 5, Appli Sequence 37, Appli Sequence 37, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 20, Appli Sequence 20, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

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; ORGANISM: Zea mays US-09-183-959-10
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Windows 95
SEQ ID NO 10
LENGTH: 515
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Best Local :
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CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
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KEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSS
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Pred. No. 7.3e-128;
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US-09-350-268-2
; Sequence 2, Application US/09350268
; Patent No. 6211433
; GENERAL INFORMATION:
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US-09-183-959-2
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Patent No. 6303332
GENERAL INFORMATION:
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Best Local Similarity
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EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: No. 6303332ember 5,
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APPLICANT: Miao, Guo-Hua
APPLICANT: Miao, Guo-Hua
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
FILE REFERENCE: BB-1125
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SOFTWARE: Microsoft Windows 95
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US-09-183-959-12
US-09-183-959-12
Sequence 12, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Maiao, Guo-Hua
APPLICANT: Rafalski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
FILE REFERENCE: BB-1125
CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT APPLICATION NUMBER: 05/064,493
; EARLIER APPLICATE: No. 6303332ember 5, 1997
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TITLE OF INVENTION: Methods and Compositions to Enhance Disease Resistance TITLE OF INVENTION: In Plants
FILE REFERENCE: 5718-42A-- Mlo3
CURRENT FILING DATE: 1999-07-06
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2
LENGTH: 496
TYPE: PRT
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Best Local Similarity
Matches 182; Conserv
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FEATURE:
OTHER INFORMATION: Mlo3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSLEYQFANDPARFRFTHQTSFVK-RHIGLSSTPG-IRWVVAFFRQFFRSVTKVDYLTLR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---VDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETET 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLVVSQD-LIQKICIDDSLMEHWMPC-RGASATASAHYGVSSSSSSSSSSAVGGGRRMLKGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIPLVILLCVGTKLEMIIMEMALEIQDR--ASVIKGAPVVEPSNKFFWFHRPDWVLFFIH 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGFVMEHFRGHPKFNFYDYMIKALEKDFKRVVSIKWYYWIFVMIFLLLNVTGWHSYFWIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWIS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTIQQEGSSAPKMIARVQKIRFIQDRCKGYEKAAWVIIWLRSFFKQFYGSVSNDDYIAMR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAFGHCSSKGKVPLLSLHALEQVHIFIFVLAITQVVLSVATVLLGLLQMRIWMHWE--- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKY----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                MGSSFKSAVFVDDVADNLRGWADGARRRVR-RSATGVDASCLGTPAAAGRG-----WEGA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIG-DATPSRGSSPMPSRGS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILEQNAFEEAYFFWTLAMFGANSCIMDSLGYSVSRIIICVVVQVLCSYSTLPLYAIVSH 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVPLALLLIGTKLEHIINRLAYEVASKHAAGQGEGGIVVSPSDELFWFRSPRLVLVLIH
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                                                                                                                                                                                                                                                                                                                                                                   AGWRLI --- AGRPSRPTQQPRS 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92; Mismatches 183;
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; NUMBER OF SEQ ID NOS: 20
; SOSTWARE: Microsoft Windows 9
; SEQ ID NO 12
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Zea mays
US-09-183-959-12
                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Windows 95
SEQ ID NO 8
LENGTH: 509
TYPE: PRT
ORGANISM: Zea mays
US-09-183-959-8
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mao, Guo-Hua
APPLICANT: Taramino, Graziana
APPLICANT: Taramino, Graziana
APPLICANT: Taramino, CORN CONA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
FILE REFERENCE: BB-1125
FILE REFERENCE: BB-1125
FILE REFERENCE: BB-1125
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09183959 Patent No. 6303332
                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                       Matches 155;
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: No. 6303332ember 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RFTHQTSFVKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFD
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YEYGMDSCFNDSEEFVFARLCLGVVVQVLCSYVTLPLYALVSQMGSTMKQSIFDEQTSKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKA 419
ALDKNMFGGQRLHVCGEGHEPFVSYEGLEQLHRFLFILGITHVLYSFVTVVLSMIKIYSW
                   S------KYVDYCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTW 159
                                                             REELMLLGVISLLLSQTA-RFISEICVPSSLFTSRFYICSESDYQDLL----RNTDANQT 112
                                                                                          KAELMLVGFISLLLIVTQDPIIAKICI-----
                                                                                                                         Conservative
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                                                                                                                                                                                                     26.2%;
                                                                                                                                                                                     101; Mismatches 162;
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                                                                                              --SEDAADVMWPCKRGTEGRKP 107
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US-09-183-959-14
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Patent No. 6303332
GENERAL INFORMATION:
Sequence 4, Application US/09183959

Patent No. 6303332

GENERAL INFORMATION:
APPLICANT: Calboon, Rebecca E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Taramino, Graziana
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
FILE REFERENCE: BB-1125
CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cahoon, Rebecca E.
APPLICANT: Miao, Guo-Hua
APPLICANT: Miao, Guo-Hua
APPLICANT: Rafialski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
FILE REFERENCE: BB-1125
CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: No. 6303332ember 5, 1997
NUMBER OF SEO ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 FPLYALVTOMGSNMKRSIFDEQTSKALTNWRNTAKEKKK 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 KKWETETTSLEYQFANDPARFRFT----HQTSFVKRHLG--LSSTPGIRWVVAFFRQFFR 213
                                                                                                                                                                                                                                                                                                                                                                 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIODRASVIKGAPVVEPSNKFFWFHR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLD 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHGINIYFWLSFVPVILVLLVGTELQHVIAQLALEVAEATAPYVGSQ-LKLRDDLFWFGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPLNVIISQMGPKFKKSLVSENVRESLHSWCKRVKDRSR 445
                                                                                                                                                                                                                                                                                             85;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.1%; Score 478; DB 4; Length 114; 74.6%; Pred. No. 3.2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 4
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Zea mays
US-09-183-959-4
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US-09-183-959-6
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; LOCATION: (4)
US-09-183-959-6
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                                                                                                                                                                                sequence 2, Application US/09323873A
Patent No. 6329503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Windows 95 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Miao, Guo-Hua
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
FILE REFERENCE: BB-1125
CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: No. 6303332ember 5, 1997
NUMBER OF SEQ ID NOS: 20
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              APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Kahan Leong
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cahoon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 52
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 LLCVGTKLEMIIMEMALE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LLIVGAKLEHIITRLAQE 78
REFERENCE: 129.16USU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09183959
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    46.2%;
                                                                                                                                                                                                                                                                                                                                                                                  Score 129; DB 4; Length 52; Pred. No. 8.1e-07; 8; Mismatches 20; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-323-873A-2
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                                                                                                  ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-245-041-15
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Best Local S
Matches 68
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Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                       SEQ ID NO 15
LENGTH: 2787
                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY FILE REFERENCE: 7853-136
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER FILING DATE: 1998-07-21
EARLIER FILING DATE: 1998-07-21
EARLIER FILING DATE: 1998-10-20
NUMBER: 60/104,978
EARLIER FILING DATE: 1998-10-20
NUMBER: OF SEQ ID NOS: 131
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PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Moore, K. APPLICANT: Nagle, D.
                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 ILVINKV---LPMVS-ITLLALVYLPGVIAAIV------QLHNGTKYKKEPHWLD- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 TLIWISFIPLVILL 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALS-----RLKMRTWKKWETET 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSLEYQFANDPARFRFTHQTSFV----KRHLGLSSTPGI----RWVVAFFRQFFRSVTKV 218
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      Conservative
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                       3.2%;
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      64;
                     Score 90.5;
Pred. No. 6.
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      Mismatches 190;
                                            DB 4;
                                          Length 2787;
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      Indels 137;
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1780 HASLSRKEHEHLGPLDQRASVCPAASSE-----LVVHSQAGVDSDARKGTASHCQAEA 1832
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                                                                                              EFSHPRNISSSRDERKAEMNELKLLFLLSKRTLSR-RRPLPPPPCHPRPDKRSEERTHSC 1779
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                                               HKGMGRSDD-----PQSAPTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEA
                                                                                                                                             ALTNWRN--TAKEKKKVRDTDMLMAQMIGDATPSRGSSPMP------SRGSSPVHLL 467
                                                                                                                                                                                                                                              PGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALV---TQMGSNMKRSIFDEQTSK 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                             VGISLPL---WGVAILTLFLDINGV------GTLIWISFIPLVILLCVGTKLEMI 301
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RESULT 12
PCT-US94-00198-4
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                                                                                          TELEFAX: (201)822-7039 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1
STREET: Madison
CITY: Mew Jersey
nsA
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3079 amino aci
                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (201)822-7255
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                      COMPUTER: Macinto OPERATING SYSTEM: SOFTWARE: Microso
                                          TYPE: amino acids
                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                         NAME: Lunn, Paul G. REGISTRATION NUMBER: 32,743
                                                                                                                                                                                                                                                                            CLASSIFICATION:
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               TOPOLOGY:
                         STRANDEDNESS:
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Microsoft Word 5.1a
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               linear
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; Sequence 2, Application US/08050684
; Patent No. 5550221
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1415
                                                             SOFTWARE: PatentIn Relicuration DATA:
                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                             APPLICANT: Johann Dr., Stephen V
APPLICANT: Van Zeijl Dr., Marja
APPLICANT: O'Hara Dr., Bryan M.
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                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Amphotropic Virus Receptor NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477
ATTORNEY/AGENT INFORMATION:
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nes 95; Conserv
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                                                                                                                                                                                                             STREET:
                              APPLICATION NUMBER: US/0 FILING DATE: 16-APR-1993
                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              COUNTRY: United States of America ZIP: 06904-0060
                 CLASSIFICATION:
                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDILYIDTAIEASTAIAYLTRHTFLEIPPAASDPELSRSRSVIFGFYFNILMKGLEKSSD 1597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FINAHLSQNSKF-DFHKYIKRSMEDDFKVVV------GISLPLWGVAILTLFLDI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWV-VAFFRQFFRSVTKVDYLTLRAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHNIEFVEAMCHDNYTTSGSIAFQRRTRNNILRFATIPNAILLDSMRMIYKKWHTYTHSK 1307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASV----IKGAPVVEPSNKFFW 330
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                                                                                                                                                                                                               Stamford
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                                                                                                                                                                                                                              1937 West Main
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                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                  American Cyanamid Company
37 West Main Street
                                                                                                                               Floppy disk
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                                                   US/08/050,684
                                                                                                                                                                                                                                                                                                                                               Stephen V.
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Pred. No. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --PSRGSSPMPSRGSSPV-----HLLHKGMGRSDD 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     374
          APPLICATION NUMBER:
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, MOLECULE TYPE: protein US-08-050-684-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-582-719-2
US-08-582-719-2
; Sequence 2, Application US/08582719
patent No. 5633348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 203-321-2361
TELEPAX: 203-321-2971
TELEX: 710-474-4059
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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ZIP: 06904-0060

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             APPLICANT: Johann Dr., Stephen V.
APPLICANT: Van Zeijl Dr., Marja
APPLICANT: O'Hara Dr., Bryan M.
TITLE OF INVENTION: Amphotropic Virus
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 TLRAGEINAHLSONSKEDEHKYIKRSMEDDEKVVVGISLPLWGVAILTLELDING----V 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 TIRKGIIDVNL-----YNETVETLMAGEVSAMVGSA--VWQLIASFLRLPISGTHCIV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 19.4 hes 78; Conservative
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                                                                                                                                                                                      CITY: Stamford
STATE: CT
                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALSMTHGSVKSPISNGTFGFDGHTRSDGHVYHTVHKDSGLYKDLLHKIHIDRGPEEKPAQ 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VSDESLSKVQEAESPVFKELPGAKANDDSTIPLTGAAGETLGTSEGTSAGSHPRAAYGR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIFDEQISKALINWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSP-----
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                                                                                                                                                                                                                                    E: American Cyanamid Company
1937 West Main Street
                                                                                                                                                                    United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.28;
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Pred. No. 1.3;
41; Mismatches
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                                                                                                                                                                                                                                                                                                                                         Receptor
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463 254 Gaps

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US/08/582,719

US-09-404-650-5

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US-09-404-650-5
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                                           FILE REFERENCE: RO043B-REG sequence listing CURRENT APPLICATION NUMBER: US/09/404,650 CURRENT FILING DATE: 1999-09-23 NUMBER OF SEQ ID NOS: 12 SOFTWARE: PATENTIN Ver. 2.0 SEQ ID NO 5 LENGTH: 1835
                                                                                                                                                                                                             Sequence 5, Application US/09404650
Patent No. 6309858
GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS;
TITLE OF INVENTION: AND USES
ETTE PERFERENCE. BOALST-BESTER TO THE PERFERENCE. BOALST-BESTER TITLE OF INVENTION: AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.2%; Score 88; DB 1; Length 652; Best Local Similarity 19.4%; Pred. No. 1.3; Matches 78; Conservative 41; Mismatches 120; Indels 164;
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ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 31937-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
TELEPHONE: 203-321-2361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A
REGISTRATION NUMBER: 31,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,684
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LENGTH: 652 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 TIRKGIIDVNL-----YNETVETLMAGEVSAMVGSA--VWQLIASFLRLPISGTHCIV 119
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TELEFAX: 203-321-2971
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                                                                                                                                                                                                                                                   COMPOSITIONS THEREOF;
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                                                                                                                                                                                                                                                                                                                                                                                                                       1509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1366 MLLYFISFLLIVSFFVLNMFVGV---VVENFHKCRQHQEAEEARRREEKRLRRLEKKRRK 1422
                                                                                   1698
                                                                                                                                                                                                                                                   1590 FIYAALGVELFGKLVCNDENPCEGMSRHATFEN-FGMAFLTLFQVSTGDNWNGIMKDTLR 1648
                                                                                                                                                                                                     366 KCYHTQ-IGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWR 424
                                                                                                                                                                                                                                                                                                                                                                              283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 PSK----YVDYCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 MLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEG------RK 106
                                                                                                                                                                  DCTHDERTCLSSLQFVSPL---YFVSFVLTAQFVLINVVVAVLMKHLDDSN-----K
                                                                                                                        NTAKEKKKVRDTDMLMAQMIGDA---
                                                                                                                                                                                                                                                                                             FIHLTL-----
                                                                                                                                                                                                                                                                                                                                      LPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLF-----MLLF
                                                                                                                                                                                                                                                                                                                                                                         ISFIPLVILLCVGTKLEMIIMEMALEIQDRA---SVIKGAPVVEPSNKFFWFHRPDWVLF 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRAGFINAHLSONSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLETALKY-----CNYMFT--TVFV------LEAVLKLVAFGLRRFFKD------ 1508
                                                                                   EAQEDAEMDAEIELEMAHGLGPCPGPCPGPCPCPCPCPCAGPRLPTSSPGAPGRGSG--- 1754
                                       LLHKGMGRSDDPQS 479
GAGAGGDTES 1764
                                                                                                                                                                                                                                                                                                                                                                                                                     ----RWNQLDLAIVL---LSVMGITLEE--IEINAA----- 1535
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                                                                                                                                                                                                                                                                                             -----FQNAFQMAHFVWTVATPG------LK 365
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8.3;
                                                                                                                             TPSRG----SSP-MPSRGSSPVH 465
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search completed: July 23, 2002, 14:25:22
Job time: 3295 sec

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No.
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Maximum DB seq length: 2000000000
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1 MSDKKGVPARELPETPSWAV.....ASSSALEADIPSADFSFSQG 533
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Listing first 45 summaries
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                                                                                                          Hordeum vulgare ML
Barley Mlo protein
Hordeum vulgare ML
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Wheat Mlo fungal r
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    Hordeum
  vulgare
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Maize MLO4 protein	AAY44603	21	509	6	2	45
mays SCLBr p	AAY14138	20	509	9	730.5	44
Zea mays SCLBr pro	AAY14140	20	264	7	ũ	43
ze MLO1 prot	AAY44601	21	224	7	765	42
MLO7	AAY44606	21	499	8	783.5	41
disea	AAU00505	22	496	œ	801.5	40
MLO3	AAY44782	21	496	8	2	39
Mlo	AAB01798	21	450	۳	886	38
-	AAB01808	21	492		_	37
()	AAY44607	21	492	_	888.5	36
Zea mays SCLBr pro	AAY14135	20	492	1	38	35
Soybean Mlo homolo	AAB01794	21	187	'n	916	34
Arabidopsis thalia	AAY26971	20	526	ω	924.5	$\frac{3}{3}$
S	AAB31255	22	526	ω	927.5	32
Arabidopsis thalia	AAB03403	21	526	·	932.5	31
	AAW59446	19	526	ω	932.5	30
	AAB01793	21	506	ω	944	29
	AAG35700	21	482	5	998	28
	AAG35699	21	511	.8	1071.5	27
	AAB01795	21	530		1072	26
О	AAB01797	21	221	39.4	1098	25
Arabidopsis thalia	AAB03402	21	542	9	1100	24
V2	AAB31256	22	593	.0	1130.5	23
	AAY26972	20	593		1130.5	22
Amino acid sequenc	AAB31253	22	569		1134.5	21
	AAY26969	20	569		1134.5	20
e MLO2 p	AAY44602	21	565	۲	1160	19
Arabidopsis thalia	AAB03404	21	583	٠.	234	18
S	AAB31254	22	573	.5	1253:5	17
Arabidopsis thalia	AAG35698	21	573	Ģ	4.3	16
Arabidopsis thalia	269	20	573	<u>ب</u>	N1	15
6 prot	4460	21	515	ŗ	1257	14
mays SC	413	20	515	45.1	1257	3
Oryza sativa MLO p	AAW59444	19	536	ũ	1767.5	2

## ALIGNMENTS

RESULT AAW59442 ID AAW5 PTTT 07-MAR-1997; 29-JUL-1996; 30-OCT-1996; New isolated Mlo gene of barley - used to develop products for the production of transgenic plants which have increased pathogen resistance  $% \left( 1\right) =\left\{ 1\right\}$ AAW59442; AAW59442 standard; Protein; 533 WPI; 1998-159149/14. N-PSDB; AAV35022. Bueschges R, 29-JUL-1997; 05-FEB-1998. WO9804586-A2 Hordeum vulgare. MLO; mildew; pathogen; resistance Hordeum vulgare MLO protein 13-OCT-1998 (first entry) (INNE-) INNES CENT INNOVATIONS LTD JOHN. Ъ Panstruga 97GB-0004789. 96GB-0015879. 96GB-0022626. 97WO-GB02046 ₽, Schulzelefert PMJ; Ą

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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        WO200036110-A2
                                                      Barley Mlo protein
                                                                      27-OCT-2000
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                                                                                                                                          1;
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                                       Mlo homologue;
                       vulgare
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ilarity 100.0%;
Conservative 0;
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                                        disease
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                                                                                                                                                                                                                                                                                                                                                   533 AA;
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100.0%; Pred. No. 1.:
tive 0; Mismatches
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No. 1.1e-293;
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29-JUL-1996;
30-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bueschges R,
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                                                                                                                       LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
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                                 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
                                                                         rfthqtsfvkrhlglsstpgirwvvaffrqffrsvtkvdyltlragfinahlsqnskfdf 240
                                                                                        RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
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96GB-0015879.
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                                                                                                                                                                                                                                                                       99.8%;
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Pred. No. 4.8e-293;
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126

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Matches Query Match Best Local :

Local Similarity

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Conservative

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Score 2434; D Pred. No. 3.2e 20; Mismatches

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                  The present sequence is a putative protein sequence for a Mlo homologue from wheat. Its coding sequence was identified by searching a root and leaf cDNA library for sequences encoding proteins similar to Mlo from Hordeum vulgare (barley) and Arabidopsis thaliana. Mlo confers resistance to Erysiphe graminis f. sp. hordei upon the plant, and its inactivation leads to the prining of disease resistance vote to present. The gene and protein can be used to create transgenic plants which have increased disease resistance, as well as allowing researchers to find other resistance-conferring genes and proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB01805 standard;
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   AA;
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This sequence represents the wheat fungal resistance protein TrMlol, which confers resistance to fungal pathogens by stimulating the formation of large cell wall appositions, designated papillae, at the contact site with the fungal pathogen. These papillae mainly contain callose, but also contain carbohydrate, phenols and proteins and are used to prevent penetration of the fungal hyphae into the plant. The new Mio sequences
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                                                                                                                                                                                                                               sp.
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                               98US-0042763.
                                                                                                        99WO-EP01779
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88.2%;
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callose; carbohyd;
                                                                                                                                                                                                                                                                      callose; carbohydrate; powdery mildew.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534
                                                                                                                                                                                                                                                                                                                                                            protein TrMlo3.
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Pred. No. 4
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                                                                                                                                                                                                                                                                                               apposition;
sgenic plant;
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Best Local
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N-PSDB; AAZ30411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the wheat fungal resistance protein TrMlo3, which confers resistance to fungal pathogens by stimulating the formation of large cell wall appositions, designated papillae, at the contact site with the fungal pathogen. These papillae mainly contain callose, but also contain carbohydrate, phenols and proteins and are used to prevent penetration of the fungal hyphae into the plant. The new Mlo sequences are used to generate transgenic plants resistant to fungal pathogens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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 Amino acid sequence of the wheat Mlo protein TrMlol.
                     20-APR-2001
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                                                                                                                                                                                                                                                                                       SCHOLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYOFANDPARFRFTHQ 185
                                                                                                                 GFISLLLIVTODPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG 125
                                                                                                                                                                                                  dcfhmniglsimkvvlglalqflcsyitfplyalvtqmgsnmkrsifdeqtakaltnwrn
                                                                                                                                                                                                                KCYHTQIGLSIMKVVVGLALQFLCSYMTEPLYALVTQMGSNMKRSIFDEQTSKALTNWRN
                                                                                                                                                                                                                                                                                                                                              TSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIK 245
                                                                                                                                                             takekkkvrdtdmlmaqmigdatpsrgtspmpsrgsspvhllqkgmgrsddpqsaptspr
                                                                                                                                                                      TAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPR 485
                                                                                                                                                                                                                                                                                                                                    tsfvkrhlglsstpgvrwvvaffrqffrsvtkvdyltlragfinahlsqnskfdfhkyik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 68-70;
                                                              standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2433; DB 20;
Pred. No. 4.1e-255;
22; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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Best Local Similarity
Matches 470; Conserv
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Vernooij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 90-92;
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DB; AAF24583.
NOVARTIS-ERFINDUNGEN VERW
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Heifetz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fungal pathogen; Erysiphe graminis;
wall apposition; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                           Score 2433; DB 22;
Pred. No. 4.1e-255;
2; Mismatches 37;
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Vernooij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                              Local Similarity
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                                                                                       gfislllavtqdp-isgicisqkaasimrpck-vepgsvkskykdyycakegkvalmstg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide which encodes Mlo protein from wheat, useful for cing fungal resistant plants, in particular wheat plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NOVARTIS AG.
) NOVARTIS-ERFINDUNGEN VERW GES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 99-101;
                                                                                                                                                                                                                                                                                                        534 AA;
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weislo LJ,
Levin JZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance;
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                                                                                                                                                                                                            87.3%;
88.8%;
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Heifetz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungal pathogen;
wall apposition;
                                                                                                                                                                                     22;
                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                  Score 2433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apposition;
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                                                                                                                                                                                                              No.
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Patton
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                                                                                                                                                                                                              4.1e-255;
                                                                                                                                                                                                                                  DB 22;
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Que Q;
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                                                                                                                                                                                                                                                                                                                       Mlo;
                                                                                                                                                                                                                                                                                                                                 Consensus; resistance; papilla; contact site;
                             Claim
                                                 New proteins useful fungal infection -
                                                                                 N-PSDB;
                                                                                                              Salmeron JM,
                                                                                                                            (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                   Triticum sp
                                                                                                                                                                                                                                                                                                                                                               Wheat Mlo fungal resistance protein TrMlo2
                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                             AAY26967 standard;
                                                                                                                                                                 17-MAR-1998;
                                                                                                                                                                                    17-MAR-1999;
                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                1999-571820/48
DB; AAZ30410.
                                                                                                                                                                                                                                                                                                                       Erysiphe graminis;
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                             2; Page 63-65; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                              Weislo
                                                                                                                                                                98US-0042763
                                                                                                                                                                                     99WO-EP01779
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                            /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                                               fungus; pathogen; wheat; cell wall; apposition;
callose; carbohydrate; phenol; transgenic plant
                                                                                                                                                                                                                                               "encoded by GYC"
                                                            generating transgenic plants resistant
                                                                                                                                                                                                                                                                                                                       powdery mildew.
                                                                                                               Strawn LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534
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This sequence represents the wheat fungal resistance protein TrMlo2, which confers resistance to fungal pathogens by stimulating the form

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
28-DEC-2000
              WO200078799-A2
                                  Key
Misc-difference
                                                                    powdery
                                                                            Wheat; fungal
                                                                                        Amino acid sequence of the wheat Mlo protein TrMlo2.
                                                                                                                                   AAB31251 standard; Protein;
                                                                                                                                                                      487
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                                                                                                                                                                                                                                                                                 PARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLV
                                                                    mildew;
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                       (first
                                                                   resistance; fungal pathogen;
w; Mlo; cell wall apposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                 Location/Qualifiers
                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  87.2%;
                            "unspecified
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Pred. No. 5.3e-255;
20; Mismatches 33;
                            amino
                            acid
                                                                   Erysiphe graminis;
transgenic plant.
                            encoded
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Best Local S
Matches 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 94-96; 128pp; English.
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les 471; Conserv
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DB; AAF24584.
GFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG
                                                                  gfislllavtqdp-isgicisekaasimrpcsl-ppgsvkskykdyycakkgkvslmstg
                                                                                      KCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide which encodes cing fungal resistant plants,
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                                                                                                                                                                                                                                                                                                                    Conservative
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Levin J
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                                                                                                                                                                                                                                                                                                                           87.2%; Score 2432; DB 22;
89.2%; Pred. No. 5.3e-255;
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Heifetz
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Patton
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Best Local S
Matches 379
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29-JUL-1996;
30-OCT-1996;
                                                                                                                                                                                                                                                                                                                    The sequence is that encoded by a homologue of the MLO gene, wild-type MLO exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of MLO function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance, especially resistance to powdery mildew or rust. The product can also be used for identifying compounds able to stimulate a defence response in a plant by interaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare MLO protein homologue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLO; mildew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Mio gene of barley – used to develop products for the production of transgenic plants which have increased pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bueschges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig 14; 150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INNE-) INNES
                                     187
                                                            164
             224
                                                                                    127
                                                                                                          111
                                                                                                                                  83
                                                                                                                                                        70
                                                                                                                                                                                                       10
                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-159149/14.
                                                                                                                                                                                           RELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGF 69
RAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLMGVAILTLFLDINGVGTLIWI
                                 -----VDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWE
                                                                                                                                                                             relsdtptwavavvcavmilvs vame halh klghwfhkwrk kalgealekm kaelmlvgf
                                                                                 ISLLIVTQDPIIAKICISEDAADVMWPCK-----RGTEGRKPSKY------
                                                                                                                                 ||||||||||| :::||||::| : | |||
| islllivtqdp-vsriciskeagekmlpckpydgagggkgkdnhrrllwlqgesethrrf 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV35030
                                                                                                                                                                                                                                                                                                           polypeptide.
                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽,
                                                                                                                                                                                                                                                                                     544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogen;
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97GB-0004789.
96GB-0015879.
96GB-0022626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Panstruga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-GB02046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                        69.1%;
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                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schulzelefert
                                                                                                                                                                                                                              Score 1927; DB 19;
Pred. No. 4.3e-200;
1; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMJ;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                      544;
                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                              Gaps
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RESULT 1
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 07-MAR-1997;
29-JUL-1996;
30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW59444 standard;
                                   The sequence is that encoded by a homologue of the MIO gene, wild-type MIO exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of MIO function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance, especially resistance to powdery mildew or rust. The product can also be used for identifying compounds able to
                                                                                                                                                                                                                                                                                                                                                               MLO; mildew;
                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW59444;
                                                                                                                                                                                                                                                                                  29-JUL-1997;
                                                                                                                                                                                                                                                                                                                        WO9804586-A2
                                                                                                                                                                                                                                                                                                                                          Oryza sativa
                                                                                                                  Claim 5; Fig
                                                                                                                                            New isolated Mlo gene of barley - used to develop products for production of transgenic plants which have increased pathogen
                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                      Bueschges R,
                                                                                                                                                                                                                        (INNE-)
Sequence
                  encoded
                             The product can also
stimulate a defence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vhllhkagarsddpqsvpaspraekeggg----vqhparkvppcdgwrsasspaldahi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSADFSFS
                                                                                                                                                                                    1998-159149/14.
                                                                                                                                                                                                                          INNES
                   polypeptide
 536
                                                                                                                                                                                                                                                                                                                                                               pathogen; resistance
                                                                                                                                                                                                                                                                                                                                                                                 MLO protein
                                                                                                                  13; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
                                                                                                                                                                                                      Panstruga
                                                                                                                                                                                                                          CENT INNOVATIONS LTD JOHN.
                                                                                                                                                                                                                                           97GB-0004789.
96GB-0015879.
96GB-0022626.
                                                                                                                                                                                                                                                                                   97WO-GB02046
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                              response
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                                                                                                                                                                                                        Schulzelefert PMJ
                              in a plant by
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                              interaction
                               with
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Best Local
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  WPI; 1999-313350/26
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                                                                                                                                                                                                                                                                                                                                                                                       fungus;
                                                                                                                                                                                                                                                                                                                                                                                                              SCLBr protein;
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                                                                                                                                               05-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                            Zea mays
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                                                                                               PONT DE NEMOURS & CO
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                                               Miao G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            southern corn leaf blight resistance; leaf blight disease; thosporium maydis; corn; resistance.
                                                                                                                                               97US-0064492
                                                                                                                                                                                               98WO-US23195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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                                                  Rafalski JA,
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RESULT 1
AAY44605
ID AAY4
XX
AC AAY4
XX
DT 07-P
XX
MI.00
KW MI.00
KW dise

(first

Maize MLO6 protein

AAY44605 standard; Protein; 515

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MLO6 protein; ZmMLO6; chromosome 5; mutation; disease resistance; pathogen; anti-infective;

recessive allele; antipathogenic; a

antiviral;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is a southern corn leaf blight resistance (SCLBr) protein of the invention. A chimeric gene containing the SCLBr coding sequence, can be used to alter the level of expression of a SCLBr protein in a host cell. The nucleic acid fragments can be used as probes, or to synthesize primers, to obtain further nucleic acid fragments or homologues encoding all or a substantial portion of the amino acid sequence encoding a SCLBr protein. The polynucleotides are useful for the production of transgenic plants having altered resistance to certain diseases, such as leaf blight disease caused by the fungus Helminthosporium maydis in corn (Zea mays).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX58274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                      VKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRS
                                                                                                                                                                                                                                        OLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSF
                                                                                                                                                                                                                                                                                      a \verb|vavpgkkkk| a \verb|aaaaad | hlggvvdwpppyyahnarmlae as \verb|matkcpegkvplisinalh| \\
                                                                                                                                                                                                                                                                                                                                 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK-----RGTE------
                                                                                                         EIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKC
                                                                                                                                                                                        kkkaptgg----skhggggsptaggsptkadgda
                                              ----GRKPSK-----YVDY-----
                KEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 44-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding southern corn leaf blight resistance protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1257; DB 20;
Pred. No. 2.6e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                            462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 515;
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Zea

Кеу

Location/Qualifiers

antifungal;

antihelminthic; anti-arthropod; maize; HvMLO1

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Query Match 45...
Best Local Similarity 48...
Matches 251; Conservative
                                                                                                                        The present sequence is the maize MLO6 (ZmMLO6) protein, which exhibits sequence homology to barley MLO1 (HvMLO1) sequence. MLO6 protein is encoded by a mutation-induced recessive allele MLO6, located on chromosome 5, that confers resistance to plant pathogens. Expression of native MlO genes in plants can be altered by transforming them with a DNA construct comprising the mutated Mlo gene. Decreasing the expression or activity of native MLO protein leads to enhanced resistance of plants against pathogens such as fungi, virus, nematodes and insects. Mlo gene
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                                                                                                                                                                                                                                                    Creating or enhancing disease resistance resistance genes expression .
                                                                                                                                                                                                                                                                                                                                              (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                            07-JUL-1999;
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                                                                                                                                                                                                                               Claim 1b; Page 71-73; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                     07-JUL-1998;
                                                        Sequence
                                                                            can be used to isolate related sequences from other plants and as molecular markers used in breeding programs aimed at improving disresistance. MIO protein has anti-infective, antipathogenic, antiviantifungal, antihelminthic and anti-arthropod activity.
                                                                                                                                                                                                                                                                                                  2000-137196/12
                                                                                                                                                                                                                                                                                       AAZ49564
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460..515
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190..209
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 84;
Score 1257; DI
Pred. No. 2.6e:
84; Mismatches
            DB 21;
.6e-127;
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   Indels
                        Length
                                                                                                                                                                                                                                                                   by modulating plant
                          515;
   64;
                                                                                            antiviral,
                                                                                                         disease
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GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65

Claim 3;

Page 78-81;

102pp; English.

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                                                                                                                                                                                                           Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition; papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
                                                                                                                                                                                                                                    Arabidopsis thaliana fungal resistance protein CIB10295
                                                                                                                                                                                                                                                                                        AAY26970 standard; Protein;
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                                                                          Salmeron JM,
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                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                     Mlo; Erysiphe graminis;
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                                                         WPI; 1999-571820/48
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                       fungal infection
                              New proteins useful
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NOVARTIS-ERFINDUNGEN VERW GES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the Arabidopsis thaliana fungal resistance protein CIBIO295, which confers resistance to fungal pathogens by stimulating the formation of large cell wall appositions, designated papillae, at the contact site with the fungal pathogen. These papillae mainly contain callose, but also contain carbohydrate, phenols and proteins and are used to prevent penetration of the fungal hyphae into the plant. The new Mio sequences are used to generate transgenic plants resistant to fungal pathogens, especially Erysiphe graminis (powdery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                          SVITIALSRLKMRTWKKWETETTSLEYOFANDPARFRFTHQTSFVKRHLGL-SSTPGIRW 203
VHRL-NPNDRRRSASSS-----ALEADIP------SADFSFSQ 532
                                                                                                                                   vqpgddlfwfgkprfilflihlvlftnafqlaffawstyefnlnncfhestadvvirlvv 417
                                                                                                                                                                                                                                     VEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVV 381
                                                                                                                                                                                                                                                                      :| ||:| | : |: :|: |||||::| ||||||:|| :: | ||:: |::|||| iwfvavlflltnsyglrsylwlpfiplvvilivgtkleviitklglrigekgdvvrgapv
                                                                                                                                                                                                                                                                                                      LWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPV 321
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                                                                                                                                                                                                                                                                                                                                                                                                         civtyafgkikmrtwksweeetktieygysndperfrfardtsfgrrhlnfwsktrvtlw 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dkpgrrlllelaesyihrrslatkgydkcaekgkvafvsaygihqlhififvlavvhvvy 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSK------ 109
                                                                   rhsgsntpfssrpttpthgsspihllhnfnnrs--venypsspsprysgh-----ghh
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Search completed: July Job time: 3432 sec 23, 2002, 14:24:34

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Run on:
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                                                                                                                                                 696.8
583.2
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556
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402.2
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343.2
284.8
253
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B1954631 HVSMEm001
B1808093 C002D08 00
BG904890 Talr1135F
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BG642916 EST511110
B1432930 EST535691
AW934153 EST35996
BM080281 MEST106-D
BF729342 1000076C0
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## ALIGNMENTS

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RESULT BE519781 JOURNAL COMMENT ACCESSION VERSION KEYWORDS REFERENCE AUTHORS SOURCE DEFINITION FEATURES TITLE ORGANISM source BE519781 700 bp mRNA linear EST 23-OCT-2001 HV\_CEb0021D05f Hordeum vulgare seedling green leaf EST library HYcDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone HY\_CEb0021D05f, mRNA sequence. Unpublished (2001)
On Aug 8, 2000 this sequence version replaced gi:9743969
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library. Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae

Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae Email: rwing@clemson.edu Total hq bases = 586 Seq primer: AATTAACCCTCACTAAAGGG BE519781.2 Tel: 864 656 7288 Fax: 864 656 4293 barley. Triticeae; Hordeum. (bases 1 to 700) quality sequence start: 4 quality sequence stop: 664.
Location/Qualifiers /organism="Hordeum vulgare" /cultivar="CI16151 (Mla6)" /db\_xref="taxon:4513" /clone="HV\_CEb0021D05f" GI:13266203

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Query Match
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gtcgtcgtcggcatcagcctcccgctgtggggtgtgggcgatcctcaccctcttccttgac
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library HVcDNA0005 (Blumeria challenged)"
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                                       GTGGCCACGCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCATGAAG
ctcgtcacacagatgggatcaaaacatgaagaggtccatcttcgacgagcagacgtccaag
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AV945501
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato,K., Saisho,D. and Takeda,K. Barley EST sequencing project in Unpublished (2002)
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/db_xref="taxon:77009"
/clone="bah26013"
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                                                                                                                                                                                                                                                               submission;
database:http://www.shigen.nig.ac.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  Contact: Kazuhiro Sato
Research Institute for Bioresources
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato.K., Saisho,D., Takeda,K., Shini,T. and Koh
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Unpublished (2001)
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vulgare subsp. spontaneum
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/clone="bah26013"
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BE558835
                                                                                                                                                                   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., E Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simm,D.W., Fenton,R.D., Oates,R. and Main,D. Development of a genetically and physically anchored for barley genomics: Blumeria infected incompatible (leaf cDNA library
Email: rwing@clemson.edu
Total hg bases = 458
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                     Unpublished (2001)
On Aug 14, 2000 this sequence version replaced
                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea; Triticeae; Hordeum.

1 (bases 1 to 798)
                                               Tel: 864 656 7288 Fax: 864 656 4293
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/clone_lib="Hordeum vulgare seedling green
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/tissue_type="seedling green leaf"
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/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
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WWR06.F5R000101 ITEC WWR Wheat
Clone WWR06.F5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Hermann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 601
                                                                                                                                                                                                                                                                                                                    Email: wolfgang.schuch@aguk.zeneca.com
International Triticeae EST Cooperative
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   Zeneca Wheat Improvement Centre, Norwich Research Park
Colney Lane, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 250 2600
Fax: 44 1603 250 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Schuch W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae
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                                                                                                                                                                121
                                                                Conservative
                                                                                                                                                                             /note="M13 clone. "
                                                                                                                                                                                                                                          /organism="Triticum aestivum"
/cultivar="Novosibirskaya 67"
/db_xref="taxon:4565"
/clone="WWR06.F5"
                                                                                                                                                                                                          /clone_lib="ITEC WWR Wheat Root Library"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                              . 613
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BE405256
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Contact: Olin Anderson
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 510559573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fo, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Seaton,C.L. and Tong,J.C.
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                                                                                                                                                                                                                                                                                                                                           quality sequence with phred score
Seq primer: Strategene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
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/dev_stage="Five day old etiolated
/lab_host="E. coli SOLR"
                                                                                                                                                                     /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1210_E11_I22"
                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
/note="Vector: Lambda Uni-ZAP XR,
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AV945620 TRNA 1 inear EST 18-JAN-2002

AV945620 RRNA 1 inear EST 18-JAN-2002

AV94562
                                                                                             Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeau;
Triticeae; Hordeum.
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1 (bases 1 to 402)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.1%;
87.9%;
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Pred. No. 8.9e-68;
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                                                                                                                      bread wheat.

Triticum aestivum

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeau;

Triticeae; Triticum.
Unpublished (2001)
Contact: Dr. Sylvie Cloutier
                                                  Cloutier, S., Dong, G. and Walsh, A. Wheat functional genomics Thatch
                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BG904891
                                                                                                                                                                                                                                                                                                                                                                                      BG904891 490 bp mRNA linear EST UST-
Talr1135F04F Talr1 Triticum aestivum cDNA clone Talr1135F04
                                                                                                                                                                                                                                                                                                            BG904891.1 GI:14312567
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Location/Qualifiers
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/db_xref="taxon:77009"
/db_nref="taxon:77009"
/clone=lib="K. Sato unpublished cDNA library,
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                                                                                                                                                                                                                                                                                                                                                                                                                           tggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggg 1378
                                                                                                                                                                                                                                       aagccgacatccccagtgcagatttttccttcagccagggatga 1602
                                                                                                                                                                                                                                                                                                            acccggtgcacagactaaatcctaacgacaggaggtgcgtccgcctcgtcgtcggccctcg 1558
                                                                                                                                                                                                                                                                                                                                                                            cgcccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgc 1498
                                                                                                                                                                                                                         ATGTCGACATTCCCAGCGCAGATTTTTCCTTCAGCCAAGGATGA
                                                                                                                                                                                                                                                                                                                                                              CGCCAACCTCGCCAAGGGCCATGGAGGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGC
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                                                                                                                                                                                                                                                                                            366;
                                                                                                     HVCDNA0014 (Blumeria infected)
                                                                     BI954631
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 Hordeum vulgare
                                                     BI954631.1
                                                                                       HVSMEm0018P07f, mRNA sequence.
                   barley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="laaf tissue"
/tissue_type="laaf tissue"
/dev_stage="14 Days old"
/lab host="E. coli XLOLR"
/note="vector: Lambda LapII; mass excised in plasmid
/note="vector: Lambda LapII; mass excised in plasmid
vector pBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI
mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avr1."
a 143 c 130 g 127 t
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/cultivar="Thatcher Lr1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="TaLr1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4565"
/clone="TaLr1135F04"
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Pred. No. 2.1e-56;
0; Mismatches 38
                                                                                                         Hordeum vulgare cDNA clone
                                                                                                                       green seedling EST library
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                                                                                                                                          mRNA
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Development of a genetically and physically anchored EST resource for harley genomics: Blumeria infected Morex (compatible) seedling
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clemson University
Clemson Hall, Clemson, SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Total hq bases = 236
Seq primer: AATTAACCCTCACTAAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                  129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // Anotes "Wector: pBluescript SK(-); Site_1: EcoRI; Site_2: // Notes "Wector: pBluescript SK(-); Site_1: EcoRI; Site_2: // Notes "Wector: pBluescript SK(-); Morex (mla) plants were greenhouse grown in the R Wise lab at lowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria graminis f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frozen (Wise). In the TJ Close lab at the University of Callifornia, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of bred value 20 or
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                            this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 185 c 258 g 113 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Hordeum vulgare green seedling EST library
HVcDNA0014 (Blumeria infected)"
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/db_xref="taxon:4513"
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83.2%;
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Pred. No. 4.1e
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4.1e-45;
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              atgatcatgatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggggcc 957
CGCACCCTTATCTGATTCGTGTGTGCCACTCGTCACCTCAGTGTGGTTGGACAACTGGAG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Dong HT
Laboratory of Functional Genetics
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.Ching
Tel: 0086-571-86892051
Fax: 0086-571-86961525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 773)
Dong, H.T., Li,D.B., Zhuang, X.F., Dai,C.G.,
H.F., Jiang, Y.X., Yu,F.C., Gao,Q.K. and Ka
A Gene Expression Screen in Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                    Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer
Location/Qualifiers
                                                                                                                      Conservative
                                                                                                                                                                                                                /dev_stage="Mature stage"
/note="Vector: pSport2"
209 c 217 g 169
                                                                                                                                                                                                                                                                           M.grisea"
                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="C002D08"
                                                                                                                                                                                                                                                                                             /clone_lib="Oryza sativa mature leaf library induced
                                                                                                                                                                                                                                                              /tissue_type="leaf"
                                                                                                                                      15.8%;
                                                                                                                                      Score 253; DB 10;
Pred. No. 5.7e-39;
                                                                                                                         Mismatches 185;
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                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideau; Triticeae; Triticum.

1 (bases 1 to 518)

Cloutier,S., Dong,G. and Walsh,A.
Wheat functional genomics- Thatcher Lrl cDNA library
                                                                                                                                                                                                                                                                                                                                                   BG904890 518
Talr1135F04R Talr1 Triticum
                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BG904890
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EST.
                                                                                                              Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
                                                                                                                                                                  Unpublished (2001)
Contact: Dr. Sylvie Cloutier
                                                                                                                                                                                                                                                                        Triticum aestivum
                                                                                                                                                                                                                                                                                     bread wheat
                                                                          was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
                                                 primer were from the 5' end (so
Average inset size is >2.2 kb
Plate: 135 row: F column: 04
                                                                                                    Email: scloutier@em.agr.ca
                                    te: 135 row: F colu
primer: M13 Reverse.
1. .518
/organism="Triticum aestivum"
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                       Location/Qualifiers
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aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV835211 K. Sato unpublished cDNA library: Hordeum vulgare subsp. spontaneum top three leaves adult, heading stage Hordeum vulgare subsp. spontaneum cDNA clone bah27g01, mRNA sequence.

AV835211 AV835211 AV835211 AV835211
                                                                Contact: Kazuhiro Sato
Research Institute for Bioresources
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Ja
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato,K., Saisho,D., Takeda,K., Shini,T. and
                                                                                                                                                                                                                                                                                                                Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea; Triticeae; Hordeum.
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Sato
                                                  submission;
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/tissue_type="Leaf tissue"
/dev_stage="14 Days old"
/lab_host="8. coli XLOLR"
/note="Vector: Lambda ZapII; mass excised in plasmid
/note="Vector: Lambda ZapII; mass excised in plasmid
vector pBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI
mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the aviulence gene Avrl."
a 167 c 160 g 91 t
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/clone_lib="TaLr1"
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/db_xref="taxon:4565"
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79.3%;
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Pred. No. 64;
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                                                                         and Kohara, Y. Direct
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Best Local Sim
Matches 204;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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BG642916.1 GI:13777942
EST.
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Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST511110 tomato shoot/meristem Lycopersicon esculentum cDNA clone cToF26E11 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                   Clemson University
                                                                                                                                                                                                                                                                                                                                                                          Contact: CUGI
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 620)
                                                                                                                                                                                                                                                                                                         Jordan Hall, Clemson, SC 29634, USA
il: http://www.genome.clemson.edu/orders/index.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cultivar="H602"
/db_xref="taxon:77009"
/clone="bah27901"
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/organism="Hordeum vulgare subsp. spontaneum"
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/dev_stage="adult, heading stage"
120 c 146 g 82 t
                                         /note-"Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Small expanding leaves from the results of the state of the
                                                                                /db_xref="taxon:4081"
/clone="cTOF26E11"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                    taken
                                                                                                                                                                                                                    /organism="Lycopersicon
/cultivar="TA496"
                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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small expanding leaves from the growing tip were from greenhouse plants (4-6wks old TA496). Tissue mmediately frozen in liquid nitrogen."
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1.9e-29;
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1 (bases 1 to 643)
Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B. Generation of ESTs from Potato Leaves Challenged with Phytophthora intestans, Compatible Interaction
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                                                                                                                                                                                                                                                                                                      643 bp mRNA
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              tcatgaaggtggtggtggggctagctctccagttcctctgcagctatatgaccttccccc 1186
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 TTGCAAAAAT-GTTATAGGGGTGGGAGTCTTATTCCTATGCAGTTATATCACTCTTCCAC
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/tissue_type="leaf"
/dev_stage="6 week old"
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/clone="pPCAY62"
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TGTGCTTTTCTTGCTTCTGAATGTTAGCGGGTGGCAAGCATTGTTCTGGGCATCCTTAAT
                                                                                                                            gatecteaccetettecttgacateaatggggttggcacgeteatetggatttettteat 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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EST359996 tomato fruit mature green, TAMU Lycopersicon esculentum
cDNA clone cLEF58C7 5', mRNA sequence.
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100 Jordan Hall, Clemson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pericarp"
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/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
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/clone="clef58C7"
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/cultivar="TA496"
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6: /cgn2_6/ptodata/1,
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11, Appli
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1, Appli
1, Appli
11, Appli
11, Appli
18, Appli
18, Appli
19, Appli
10, Appli
11, Appli
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cctg---ggcctctccagcacccctggcatcagatgggtggtggccttcttcaggcagtt 

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tatgaatgtgctgaacaagttcccagcatcattctacatcagcaacttcttccggcagtt

ccgtctcaaaatgagaacatggaagaaatgggagacagagagaccacctccttggaatacca

767 516 707 456 647 396 587 336 Query Match
Best Local Similarity
Matches 632; Conserv

Conservative

26.5%;

Score 425.2; DB 4; Pred. No. 3.4e-85; 0; Mismatches 323;

Length 1851; Indels

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ctactgcccggagggcaaggtggcgctcatgtccacgggcagcttgcaccagctgcacgt 395

cttcatcttcgtgctcgcggtcttccatgtcacctacagcgtcatcaccatagctctaag 455

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ALIGNMENTS	US-08-449-709-12 US-08-449-699A-12 US-08-449-699A-12 US-07-901-703-1 US-08-147-023-1 US-08-206-864-1 US-08-28-78-729A-16 US-08-480-528A-3 US-08-479-666-3 US-08-463-53A-16 US-08-643-53A-16 US-08-643-53A-16 US-08-643-53A-16	US-07-989-847-5 US-08-469-411-5 US-07-841-646-12 US-08-147-023-12
	sequence 12, Appli sequence 12, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 1, Appli sequence 3, Appli sequence 3, Appli sequence 16, Appli sequence 16, Appli sequence 16, Appli sequence 16, Appli sequence 16, Appli	5, A 12,

## ; LENGTH: 1851 ; TYPE: DNA ; ORGANISM: Zea mays US-09-183-959-9 US-09-183-959-9 ; Sequence 9, Applicat: ; Patent No. 6303332 ; GENERAL INFORMATION: RESULT CURRENT APPLICATION NUMBER: US/09/183,959 CURRENT FILING DATE: 1998-11-02 EARLIER APPLICATION UNMBER: 60/064,493 EARLIER FILING DATE: No. 6303332ember 5, 1 NUMBER OF SEQ ID NOS: 20 SOFTWARE: Microsoft Windows 95 SEQ ID NO 9 APPLICANT: Cahoon, Rebecca E. APPLICANT: Miao, Guo-Hua APPLICANT: Rafalski, J. Antoni APPLICANT: Taramino, Graziana TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE FILE REFERENCE: BB-1125 Application US/09183959 Ħ

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US-09-183-959-11
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; Patent No. 6303332
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                                           Query Match
Best Local Similarity
Matches 484; Conserv
                                                                                                                                                               SOFTWARE: Microsoft Windows
SEQ ID NO 11
LENGTH: 1040
                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: No. 6303332ember 5, UNMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                APPLICANT: Cahoon, Rebecca E.
APPLICANT: Miao, Guo-Hua
APPLICANT: Rafalski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN
FILE REFERENCE: BB-1125
TITLE REFERENCE: BB-1125
                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
-09-183-959-11
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                                             Score 312; DB 4;
Pred. No. 2.8e-60;
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                                                                                                                                                                                                                                                          Sequence 13, Application Patent No. 6303332
                                                          SEQ ID NO 13
                                                                                                                                                      APPLICANT: Cahoon, Rebecca E.
APPLICANT: Miao, Guo-Hua
APPLICANT: Rafalski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF
FILE REFERENCE: BB-1125
                                                                                  CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: NO. 6303332ember 5,
NUMBER OF SEQ ID NOS: 20
               LENGTH: 538
TYPE: DNA
ORGANISM: Zea :
                                                                        SOFTWARE: Microsoft Windows
FEATURE:
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NAME/KEY: LOCATION: FEATURE:

unsure (479)

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Sequence 1, Application US/09350268

Patent No. 6211433

GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Methods and Compositions to TITLE OF INVENTION: In Plants
FILE REFERENCE: 5718-42A-- Mlo3
CURRENT APPLICATION NUMBER: US/09/350,268
CURRENT FILING DATE: 1999-07-06
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Pred. No. 1.7e-56;
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SEQ ID NO 1
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ORGANISM: Zea
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TYPE: DNA
ORGANISM: Zea mays
S-09-183-959-1
                                                                                                                                                                                                                                                                                               SEQ ID NO 1
TENGTH: 1725
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CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: No. 6303332ember 5, 1
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Miao, Guo-Hua
APPLICANT: Rafalski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
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Pred. No. 3.6e-39;
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; TYPE: DNA
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US-09-183-959-7
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Best Local Similarity
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APPLICANT: Miao, Guo-Hua
APPLICANT: Rafalski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN CDNA ENCODING
FILE REFERENCE: BB-1125
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Miao, Guo-Hua
APPLICANT: Mafalski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN CONA ENCODING SOUTH
FILE REFERENCE: BB-1125
CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: No. 6303332ember 5, 199
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                        US-09-183-959-17
                                                                                                                                                                                                               Sequence 17, Applicate Patent No. 6303332 GENERAL INFORMATION:
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                                                                                                                       SOUTHERN LEAF BLIGHT
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; TYPE: DNA; Cea mays US-09-183-959-17
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SEQ ID NO 17
LENGTH: 705
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Miao, Guo-Hua
APPLICANT: Mafalski, J. Antoni
APPLICANT: Taramino, Graziana
APPLICANT: Taramino, Graziana
ITILE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
FILE REFERENCE: BB-1125
CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/664,493
EARLIER FILING DATE: No. 6303332ember 5, 1997
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Best Local Similarity
Matches 152; Conserv
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SOFTWARE: Microsoft Windows 95
SEQ ID NO 3
LENGTH: 597
                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                             NAME/KEY:
LOCATION:
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                                NAME/KEY: unsure LOCATION: (559)
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NAME/KEY: unsure
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(538)
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(520)
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72.4%;
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Pred. No. 2.5e-17;
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CURRENT APPLICATION NUMBER: US/09/183,959
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: NO. 6303332ember 5, 199
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Windows 95
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 750
TYPE: DNA
ORGANISM: Zea mays
US-09-183-959-18
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US-09-183-959-3
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APPLICANY: Cahoon, Rebecca E.
APPLICANY: Miao, Guo-Hua
APPLICANT: Mafalski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
FILE REFERENCE: BB-1125
FILE REFERENCE: BB-1125
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Best Local Similarity
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                                                                                                                 Query Match
Best Local Similarity
Matches 105; Conserv
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                   742
                                               304 atgcaggtccatctggcccctggcaccaagtttgatttccaaaagtacatcaagcggtct 363
                                                                   682 atcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagaggtcg 741
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atggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtgggcgatc
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71.9%;
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Pred. No. 6.3e-10;
0; Mismatches 154
                                                                                                                 Score 80.4; DB 4;
Pred. No. 3.4e-09;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                               1997
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; NAME/KEY: unsure
; LOCATION: (450)
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; Sequence 5, Application US/09183959
; Patent No. 6303332
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Best Local Similarity
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SEQ ID NO 5
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                                                                                                                                                                                                                Matches 101; Conservative
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CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/064,493
EARLIER FILING DATE: No. 6303332ember 5, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rafalski, J. Antoni
APPLICANT: Taramino, Graziana
TITLE OF INVENTION: CORN CDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
FILE REFERENCE: BB-1125
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TYPE: DNA
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                   1265 actggcggaacacggccaaggagaagaaagtccgagacacggacatgct 1316
                                                                                        1205 agatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcggtcaacca 1264
                                                                                                                                                          1145 ggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgtcacac 1204
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                                                                    agatggggagctgctacaagaaggagatcttcaacgagcatgtgcagcagggcgtcctgg
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                                                                                                                                                                                                                               3.7%;
58.7%;
                                                                                                                                                                                                              0;
                                                                                                                                                                                                           Score 59; DB 4;
Pred. No. 0.00016;
0; Mismatches 71
                                                                                                                                                                                                              71; Indels
                                                                                                                                                                                                                                             Length 472;
                                                                                                                                                                                                             0;
                                                                                                                                                                                                             Gaps
                                                                      270
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US-07-988-260B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 47.8 Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: BRZEZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA to mRNA ORIGINAL SOURCE: Streptomyces N174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Hymo, Lawrence A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
 935 GGCCGCGCACGA 946
                                    375 cagcttgcacca 386
                                                                      875
                                                                                                315 caagcccagcaagtacgttgactactgcccggagggcaaggtggcgctcatgtccacggg 374
                                                                                                                                         815 CAGCTTCGGTGGCATCCGCAAGACCGCCATGAAGAAGGCCAGGACCCCCGCCCAGGGCGG
                                                                                                                                                               255 atgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccg 314
                                                                                                                                                                                                             755 GCTGGGCCAGTTCGCCTACTACGACGCCATCGTGATGCACGGCCCCGGCAACGACCCGAC 814
                                                                                                                                                                                                                                                 195
                                                                                                                                                                                                                                                                                  695 GCGCGACCGGGTCTACTTCGACCCGGCCGTCAGCCAGGCGAAGGCCGACGGCCTGCGCGC 754
                                                                                                                                                                                                                                                                                                      135 ccagcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcat 194
                                                                                                                                                                                                                                                                                                                                                       635 CACCAAGGACTGGGCGACCGCCGAAGGACACCGTCTTCCAGCAGGCCCAGAACGACGA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1100
CTTY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                                                                                                                                                                                                                                                                                                                     75 cgccatggtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggtt 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hymo, Lawrence A. REGISTRATION NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: U. FILING DATE: 19921214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                      gctggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagat 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6714627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202) 822-0944
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SYSTEM: PC-DOS 3.30
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DB 1; Length 1575;

163;

Indels

0;

Gaps

0

874

BRZEZINSKI, RYSZARD VENTION: ENZYME OF USE IN CHITOSAN 720 kb diskette LAH/3122/98214/MJW 9th Floor

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US-08-478-097A-37
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.1%;
Best Local Similarity 47.6%;
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KECK, PETER
APPLICANT: SMART, JOHN
TITLE OF INVENTION: SINGLE-CHAIN ANALOGS O
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
                                                                                                                                                        815
                                                                                                                                                                                                                                                                        144
                                                                                                                                                                                                                                                                                                            695 GCTGGTGTTTGACATCACAGCCACCAGCAACCACTGGGTGGTCAATCCGCGGCACAACCT 754
                                      324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1.1392
OTHER INFORMATION: /product- "MODIFIED OP-1 DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                      84 gctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcaccg 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: PITCHER ESQ, EDMUND R REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/478,097A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                caagtacgttgactactgcccggagggcaaggtggcgctcatgtccacgggcagcttgca 383
                                                                                                                                                                                    cttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctc 263
                                                                                                                                                                                                                                                        gcacaagaaggccctgtggggaggcgctggaggaagatgaaggcggagctcatgctggtggg 203
                                                                                                    CCTGATTGGGCGCACGGGCCCCAGAACAAGCAGCCCTTCATGGTGGCTTTCTTCAAGGC 874
CTCCAAGACGCCCAAGAACCAGGAAGCCCTGCGGATGGCCCAACAGCCCGGGCCGAGCGGGC 994
                                                                            CACGGAGGTCCACTTCCGCAGCATCCGGTCCACGGGGAGCAAACAGCGCAGCCAGAACCG 934
                                                                                                                                                                                                                                GGGCCTGCAGCTCTCGGTGGAGACGCTGGATGGGCAGAGCATCAACCCCAAGTTGGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 49.4; DB
Pred. No. 0.027;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 1392;
                                                                                                                                                                                                                                                                                                                                                                                      161;
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RESULT 13
US-08-717-294-42/c
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                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Elbing, Karen L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SEED, BRIAN APPLICANT: HAAS, JURGEN
3862
                                                                                                                                                                                                   4042 AACATGTTGGTGAAGTAGCTGGAGGCGGTGATCTGGGCGTCGCTGATGGCCCTTGCTCTCC 3983
                                                                                                                                  3982 ATGCCCAGGGGCATGCTGCAGCTGTTCAGGTCGCAGCCCATCAGCTCCATGCGCAGGGTG 3923
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                   193 atgctggttgggcttcatatccctgctcctcatcgtcacgccaggaccccatcatcgccaag 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/717,294 FILING DATE: 20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Clark --
emprest: 176 Federal Street
                                                                                                                                                                                                                        13 aaaggggtgccggcgcgggagctgccggagacgccgtcgtcgtgggcggttggcggtggtcttc 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Elbing, Karen L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4451 base pairs
                                                                                            ttccaqcaccggcacaaqaaqgccctgtgggaggcqctggagaagatgaaggcggagctc 192
                                                                                                                                                     gccgccatggtgctcgtgtcctcatggaacacgggcctccacaagctcggccattgg 132
AAGATGTTGTGCTTGATGCCGCTGCTGCCACGTTGCCGAAGAACACCATCAGGGTGCCG
                                                                  02110
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                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: DOS
FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                        double
                                                                                                                                                                                                                                                                                     3.0%;
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                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                   Score 47.6; DB Pred. No. 0.09;
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                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                      DB 3;
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Sequence 10,
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APPLICANT: OPPERM
APPLICANT: OZKAYN
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                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 600,024

FILING DATE: 18-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 599,543
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                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6:
FILING DATE: 04-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
COMPUTER: IB
                                                                                                  APPLICATION NUMBER: US 579,865 FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 6: FILING DATE: 04-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 8: FILING DATE: 20-DEC-1991
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FILING DATE: 19920221
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RUEGER, DAVID C.
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                                                                                                                                                   18-OCT-1990
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                                             20-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                US 621,988
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                                                               US 569,920
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            US 483,913
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US-08-147-023-10
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Best Local Similarity
Matches 135; Conserv
                                                                                                  Patent No. 5468845
GENERAL INFORMATION:
                                                                                                                  Sequence 10, Application US/08147023 Patent No. 5468845
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INFORMATION FOR SEQ ID NO:
                                               APPLICANT:
APPLICANT:
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LENGTH: 1004 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CEP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
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ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
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                APPLICANT:
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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RUEGER, L...
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                           OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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                                                                                 OPPERMANN, HERMANN
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48.0%;
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/product= "OP1B"
/note= "OP1B - FUSION"
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Pred. No. 0.069;
0; Mismatches 146;
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Length 1004; Indels

0;

Gaps

0;

263 446

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APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION NUMBER: US 621,988
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
                                          TELEFAX: 617/248-7100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 599,543
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
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ADDRESSEE: TESTA, HURWI
STREET: 53 STATE STREET
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                           REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELECPHONE: 617/248-7000
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APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
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MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 1004 base pair
                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 232,630 FILING DATE: 15-AUG-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                      FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
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FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
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ZIP: 02109
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                                                                                                                                                  NAME: PITCHER, EDMUND REGISTRATION NUMBER: 2
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                                                              617/248-7100
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Best Local Similarity 48.0%;
Matches 135; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                         caagtacgttgactactgcccggagggcaaggtggcgctca 364
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CTCCAAGACGCCCAAGAACCAGGAAGCCCTGCGGATGGCCA 607
                                                                 CACGGAGGTCCACTTCCGCAGCATCCGGTCCACGGGGAGCAAACAGCGCAGCCAGAACCG
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/product= "OP1B"
/note= "OP1B - FUSION"
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Pred. No. 0.069;
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Search completed: July 23, 2002, 11:27:17 Job time: 6610 sec

Hordeum vulgare ML Oryza sativa MLO g Hordeum vulgare ML Wheat Mlo homologu Soybean Mlo homolo

Maize MLO6 protein
Zea mays SCLBr pro
Maize MLO2 protein
Maize MLO1 protein
Arabidopsis thalia
Nuclectide sequenc
Zea mays SCLBr pro

Arabidopsis thalia Nucleotide sequenc Zea mays SCLBr pro

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                        This sequence represents the coding region for the wheat fungal resistance gene TrMlol. The Mlo protein confers resistance to fungal pathogens by stimulating the formation of large cell wall appositions, designated papillae, at the contact site with the fungal pathogen. These papillae mainly contain callose, but also contain carbohydrate, phenols and proteins and are used to prevent penetration of the fungal hyphae into the plant. The new Mlo sequences are used to generate transgenic plants resistant to fungal pathogens, especially Erysiphe
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Best Local Similarity
Matches 1431; Conserv
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The present sequence is a putative coding sequence for a Mlo homologue from wheat. It was identified by searching a root and leaf cDNA library for sequences encoding proteins similar to Mlo from Hordeum vulgare (barley) and Arabidopsis thaliana. Mlo confers resistance to Erysiphe graminis f. sp. hordei upon the plant, and its inactivation leads to the priming of disease resistance even if the pathogen is not present. The gene and protein can be used to create transgenic plants which have increased disease resistance, as well as allowing researchers to find other resistance-conferring genes and proteins.
  Sequence 1711 BP; 377
                                                                                                                                                                 Claim
                                                                                                                                                                                        New polynucleotide encoding a Mlo homologue polypeptide, useful for creating transgenic plants with altered levels of disease resistance
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Query Match
Best Local Similarity
Matches 1436; Conserv Conservative 82.1%; 89.8%; 0; Score 1315.2; DE Pred. No. 1e-270; 0; Mismatches 15 158; DB Indels Length 6; Gaps ņ

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                                                                                                                                                                                                                                                                                                                                                                                                            (NOVS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition; papilla; contact site; callose; carbohydrate; phenol; transgenic plant M10; Erysiphe graminis; powdery mildew; ss.
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/product= "fungal resistance protein M1o2"
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Pred. No. 1.3e-270;
1; Mismatches 158;
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RESULT
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ID AAZ3
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XX 21-D
C 21-D
C Whee
XX Cons
KW Cons
KW M10;
XX M10;
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Mlo; Erysiphe
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                                                                                                                                                                                                                                                                            Mlo
                                                s; resistance; fungus; pathogen; wheat; contact site; callose; carbohydrate; plsphe graminis; powdery mildew; ss.
                                     зp
                                                                                                                 standard;
                                                                          fungal resistance gene TrMlo3.
    Location/Qualifiers
198..1802
/*tag- a
/product- "fungal fus
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                                                        phenol;
                                                        cell wall; apposition;
henol; transgenic plant
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Best Local S
Matches 1424
                                                                                                                                                                                                                                                                                                                                                                                resistance gene TrMlo3. The Mlo protein confers resistance to fungal pathogens by stimulating the formation of large cell wall appositions, designated papillae, at the contact site with the fungal pathogen. These papillae mainly contain callose, but also contain carbohydrate, phenols and proteins and are used to prevent penetration of the fungal hyphae into the plant. The new Mlo sequences are used to generate transgenic plants resistant to fungal pathogens, especially Erysiphe graminis (powdery mildew).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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DB; AAY26968.
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                                                                                                                                                                                                                                                                              Local Similarity
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cell wall apposition; transgenic plant; ;
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29-JUL-1996;
30-OCT-1996;
  The sequence is that of a homologue of the MIO gene, wild-type MIO exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of MIO function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance, especially resistance to powdery mildew or rust. The product can also be used for identifying compounds able to
                                                                                                   Claim
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    used to develop products for
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29-JUL-1996;
30-OCT-1996;
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0; Mismatches 384;
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    used to develop products for
which have increased pathogen

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RESULT

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ID AAV35025 standard; D
XX
AC AAV35025;
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DT 13-OCT-1998 (first |
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DT 13-OCT-1998 (first |
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DT 13-OCT-1998 |
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DE Hordeum vulgare |
XX
WO9804586-A2.
XX
PN WO9804586-A2.
XX
PP 29-JUL-1997; 97W0-
PR 29-JUL-1996; 96GB-
PR 29-JUL-1996; 96GB-
PR 30-OCT-1996; 96GB-
PR 30-OCT-1996; 96GB-
PR 1998-159149/14.
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Best Local Similarity
Matches 741; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Mlo gene of production of transgenic
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                                                                                                                                                                            ttccagaacgcgtttcagatggcgcattttgtgtgtggacagt------
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                                                                                                                                                                                                                                                                                                                                                                                            ccctggagatccaggaccgggcgagcgtcatcaagggggcccccgtggtcgagcccagca
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                                                   tgtcagttaacatgggtgtcaaggcaccgagtgccgctgatgaactgctctgacggagat
                                                                                                                                                    ttccagaacgcgtttcagatggcgcattttgtgtggacagtggtacgccaccgatgaact 1768
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Pred. No. 1.2e-112;
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which have

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have increased pathoc
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RESULT 1
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ID AAAA52707
XX AAA5
XX Whea
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Pred. No. 7.

    (pos:452..455, aa:Xaa)
    (pos:503..505, aa:Xaa)
    (pos:530..532, aa:Xaa)
    (pos:557..559, aa:Xaa)

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                                                                                                                                                                                                                                                                                                            MLO6 protein; ZmMLO6; chromosome 5; mutation; recessive alleled disease resistance; pathogen; anti-infective; antipathogenic; antifungal; antihelminthic; anti-arthropod; maize; ss.
                                                                                                                                                                                                                                                                                       Zea
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ49564 standard; cDNA; 1815
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Claim 1c; Page 70-71; 88pp; English
                     Creating or enhancing disease resistance resistance genes expression -
                                                      WPI; 2000-137196/12.
P-PSDB; AAY44605.
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The present cDNA sequence (ATCC 98727) encodes maize MLO6 (ZmMLO6) protein. Mlo6 gene is mapped to chromosome 5. It is a mutation-induced recessive allele, that confers resistance to plant pathogens. Expression of native Mlo genes in plants can be altered by transforming them with a DNA construct comprising the mutated Mlo gene. Decreasing the expression or activity of native Mlo protein leads to enhanced resistance of plants against pathogens such as fungi, virus, nematodes and insects. Mlo gene molecular markers used in breeding programs aimed at improving disease resistance. MLO protein has anti-infective, antipathogenic, antivital, antifungal, antihelminthic and anti-arthropod activity.
Sequence 1815 BP; 394 A; 551 C; 502 G; 368 T; 0 other;
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Query Match
Best Local Similarity

26.5%;

DB 21;

Length

1815;

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                         gatcatctacttcctctggattctgtatgagtacggcatggactcgtgcttcaacgactc
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Search completed: July Job time: 5208 sec 23, 2002, 11:31:40